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(54) Title: OVEREXPRESSION OF MAMMALIAN AND VIRAL PROTEINS		
(57) Abstract		
<p>The invention features a synthetic gene encoding a protein normally expressed in mammalian cells wherein at least one non-preferred or less preferred codon in the natural gene encoding the mammalian protein has been replaced by a preferred codon encoding the same amino acid.</p>		

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- 1 -

OVEREXPRESSION OF MAMMALIAN AND VIRAL PROTEINS

Field of the Invention

The invention concerns genes and methods for
5 expressing eukaryotic and viral proteins at high levels
in eukaryotic cells.

Background of the Invention

Expression of eukaryotic gene products in prokaryotes is sometimes limited by the presence of
10 codons that are infrequently used in *E. coli*. Expression of such genes can be enhanced by systematic substitution of the endogenous codons with codons overrepresented in highly expressed prokaryotic genes (Robinson et al. 1984). It is commonly supposed that rare codons cause
15 pausing of the ribosome, which leads to a failure to complete the nascent polypeptide chain and a uncoupling of transcription and translation. The mRNA 3' end of the stalled ribosome is exposed to cellular ribonucleases, which decreases the stability of the transcript.

20 Summary of the Invention

The invention features a synthetic gene encoding a protein normally expressed in mammalian cells wherein at least one non-preferred or less preferred codon in the natural gene encoding the mammalian protein has been
25 replaced by a preferred codon encoding the same amino acid.

Preferred codons are: Ala (gcc); Arg (cgc); Asn (aac); Asp (gac) Cys (tgc); Gln (cag); Gly (ggc); His (cac); Ile (atc); Leu (ctg); Lys (aag); Pro (ccc); Phe
30 (ttc); Ser (agc); Thr (acc); Tyr (tac); and Val (gtg). Less preferred codons are: Gly (ggg); Ile (att); Leu (ctc); Ser (tcc); Val (gtc). All codons which do not fit the description of preferred codons or less preferred codons are non-preferred codons.

- 2 -

By protein normally expressed in mammalian cells is meant a protein which is expressed in mammalian under natural conditions. The term includes genes in the mammalian genome such as Factor VIII, Factor IX, 5 interleukins, and other proteins. The term also includes genes which are expressed in a mammalian cell under disease conditions such as oncogenes as well as genes which are encoded by a virus (including a retrovirus) which are expressed in mammalian cells post-infection
10 In preferred embodiments, the synthetic gene is capable of expressing said mammalian protein at a level which is at least 110%, 150%, 200%, 500%, 1,000%, or 10,000% of that expressed by said natural gene in an in vitro mammalian cell culture system under identical
15 conditions (i.e., same cell type, same culture conditions, same expression vector).

Suitable cell culture systems for measuring expression of the synthetic gene and corresponding natural gene are described below. Other suitable 20 expression systems employing mammalian cells are well known to those skilled in the art and are described in, for example, the standard molecular biology reference works noted below. Vectors suitable for expressing the synthetic and natural genes are described below and in
25 the standard reference works described below. By "expression" is meant protein expression. Expression can be measured using an antibody specific for the protein of interest. Such antibodies and measurement techniques are well known to those skilled in the art. By "natural
30 gene" is meant the gene sequence which naturally encodes the protein.

In other preferred embodiments at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the codons in the natural gene are non-preferred codons.

- 3 -

In a preferred embodiment the protein is a retroviral protein. In a more preferred embodiment the protein is a lentiviral protein. In an even more preferred embodiment the protein is an HIV protein. In 5 other preferred embodiments the protein is gag, pol, env, gp120, or gp160. In other preferred embodiments the protein is a human protein.

The invention also features a method for preparing a synthetic gene encoding a protein normally expressed by 10 mammalian cells. The method includes identifying non-preferred and less-preferred codons in the natural gene encoding the protein and replacing one or more of the non-preferred and less-preferred codons with a preferred codon encoding the same amino acid as the replaced codon.

15 Under some circumstances (e.g., to permit introduction of a restriction site) it may be desirable to replace a non-preferred codon with a less preferred codon rather than a preferred codon.

It is not necessary to replace all less preferred 20 or non-preferred codons with preferred codons. Increased expression can be accomplished even with partial replacement.

In other preferred embodiments the invention features vectors (including expression vectors) 25 comprising the synthetic gene.

By "vector" is meant a DNA molecule, derived, e.g., from a plasmid, bacteriophage, or mammalian or insect virus, into which fragments of DNA may be inserted or cloned. A vector will contain one or more unique 30 restriction sites and may be capable of autonomous replication in a defined host or vehicle organism such that the cloned sequence is reproducible. Thus, by "expression vector" is meant any autonomous element capable of directing the synthesis of a protein. Such

- 4 -

DNA expression vectors include mammalian plasmids and viruses.

The invention also features synthetic gene fragments which encode a desired portion of the protein.

5 Such synthetic gene fragments are similar to the synthetic genes of the invention except that they encode only a portion of the protein. Such gene fragments preferably encode at least 50, 100, 150, or 500 contiguous amino acids of the protein.

10 In constructing the synthetic genes of the invention it may be desirable to avoid CpG sequences as these sequences may cause gene silencing.

The codon bias present in the HIV gp120 envelope gene is also present in the gag and pol proteins. Thus, 15 replacement of a portion of the non-preferred and less preferred codons found in these genes with preferred codons should produce a gene capable of higher level expression. A large fraction of the codons in the human genes encoding Factor VIII and Factor IX are non- 20 preferred codons or less preferred codons. Replacement of a portion of these codons with preferred codons should yield genes capable of higher level expression in mammalian cell culture. Conversely, it may be desirable to replace preferred codons in a naturally occurring gene 25 with less-preferred codons as a means of lowering expression.

Standard reference works describing the general principles of recombinant DNA technology include Watson, J.D. et al., Molecular Biology of the Gene, Volumes I and 30 II, the Benjamin/Cummings Publishing Company, Inc., publisher, Menlo Park, CA (1987); Darnell, J.E. et al., Molecular Cell Biology, Scientific American Books, Inc., Publisher, New York, N.Y. (1986); Old, R.W., et al., Principles of Gene Manipulation: An Introduction to 35 Genetic Engineering, 2d edition, University of California

- 5 -

Press, publisher, Berkeley, CA (1981); Maniatis, T., et al., Molecular Cloning: A Laboratory Manual, 2nd Ed. Cold Spring Harbor Laboratory, publisher, Cold Spring Harbor, NY (1989); and Current Protocols in Molecular Biology, Ausubel et al., Wiley Press, New York, NY (1989).

Detailed Description

Description of the Drawings

Figure 1 depicts the sequence of the synthetic gp120 (SEQ ID NO: 34) and a synthetic gp160 (SEQ ID NO: 35) gene in which codons have been replaced by those found in highly expressed human genes.

Figure 2 is a schematic drawing of the synthetic gp120 (HIV-1 MN) gene. The shaded portions marked v1 to v5 indicate hypervariable regions. The filled box indicates the CD4 binding site. A limited number of the unique restriction sites are shown: H (Hind3), Nh (Nhe1), P (Pst1), Na (Nae1), M (Mlu1), R (EcoR1), A (Apa1) and No (Not1). The chemically synthesized DNA fragments which served as PCR templates are shown below the gp120 sequence, along with the locations of the primers used for their amplification.

Figure 3 is a photograph of the results of transient transfection assays used to measure gp120 expression. Gel electrophoresis of immunoprecipitated supernatants of 293T cells transfected with plasmids expressing gp120 encoded by the IIIB isolate of HIV-1 (gp120IIIB), by the MN isolate (gp120mn), by the MN isolate modified by substitution of the endogenous leader peptide with that of the CD5 antigen (gp120mnCD5L), or by the chemically synthesized gene encoding the MN variant with the human CD5Leader (syngp120mn). Supernatants were harvested following a 12 hour labeling period 60 hours post-transfection and immunoprecipitated with CD4:IgG1 fusion protein and protein A sepharose.

- 6 -

Figure 4 is a graph depicting the results of ELISA assays used to measure protein levels in supernatants of transiently transfected 293T cells. Supernatants of 293T cells transfected with plasmids expressing gp120 encoded by the IIIB isolate of HIV-1 (gp120 IIIb), by the MN isolate (gp120mn), by the MN isolate modified by substitution of the endogenous leader peptide with that of CD5 antigen (gp120mn CD5L), or by the chemically synthesized gene encoding the MN variant with human CDS leader (syngp120mn) were harvested after 4 days and tested in a gp120/CD4 ELISA. The level of gp120 is expressed in ng/ml.

Figure 5, panel A is a photograph of a gel illustrating the results of a immunoprecipitation assay used to measure expression of the native and synthetic gp120 in the presence of rev in trans and the RRE in cis. In this experiment 293T cells were transiently transfected by calcium phosphate coprecipitation of 10 µg of plasmid expressing: (A) the synthetic gp120MN sequence and RRE in cis, (B) the gp120 portion of HIV-1 IIIB, (C) the gp120 portion of HIV-1 IIIB and RRE in cis, all in the presence or absence of rev expression. The RRE constructs gp120IIIBRRE and syngp120mnRRE were generated using an Eag1/Hpa1 RRE fragment cloned by PCR from a HIV-1 HXB2 proviral clone. Each gp120 expression plasmid was cotransfected with 10 µg of either pCMVrev or CDM7 plasmid DNA. Supernatants were harvested 60 hours post transfection, immunoprecipitated with CD4:IgG fusion protein and protein A agarose, and run on a 7% reducing SDS-PAGE. The gel exposure time was extended to allow the induction of gp120IIIBrre by rev to be demonstrated. Figure 5, panel B is a shorter exposure of a similar experiment in which syngp120mnRRE was cotransfected with or without pCMVrev. Figure 5, panel C is a schematic diagram of the constructs used in panel A.

- 7 -

Figure 6 is a comparison of the sequence of the wildtype rat THY-1 gene (wt) (SEQ. ID. NO: 37) and a synthetic rat THY-1 gene (env) (SEQ. ID. NO: 36) constructed by chemical synthesis and having the most 5 prevalent codons found in the HIV-1 env gene.

Figure 7 is a schematic diagram of the synthetic ratTHY-1 gene. The solid black box denotes the signal peptide. The shaded box denotes the sequences in the precursor which direct the attachment of a phophatidyl-10 inositol glycan anchor. Unique restriction sites used for assembly of the THY-1 constructs are marked H (Hind3), M (Mlu1), S (Sac1) and No (Not1). The position of the synthetic oligonucleotides employed in the construction are shown at the bottom of the figure.

15 Figure 8 is a graph depicting the results of flow cytometry analysis. In this experiment 293T cells transiently transfected with either wildtype rat THY-1 (dark line), ratTHY-1 with envelope codons (light line) or vector only (dotted line). 293T cells were 20 transfected with the different expression plasmids by calcium phosphate coprecipitation and stained with anti-ratTHY-1 monoclonal antibody OX7 followed by a polyclonal FITC- conjugated anti-mouse IgG antibody 3 days after transfection.

25 Figure 9, panel A is a photograph of a gel illustrating the results of immunoprecipitation analysis of supernatants of human 293T cells transfected with either syngp120mn (A) or a construct syngp120mn.rTHY-1env which has the rTHY-1env gene in the 3' untranslated 30 region of the syngp120mn gene (B). The syngp120mn.rTHY-1env construct was generated by inserting a Not1 adapter into the blunted Hind3 site of the rTHY-1env plasmid. Subsequently, a 0.5 kb Not1 fragment containing the rTHY-1env gene was cloned into the

- 8 -

NotI site of the syngp120mn plasmid and tested for correct orientation. Supernatants of 35S labelled cells were harvested 72 hours post transfection, precipitated with CD4:IgG fusion protein and protein A agarose, and 5 run on a 7% reducing SDS-PAGE. Figure 9, panel B is a schematic diagram of the constructs used in the experiment depicted in panel A of this figure.

Description of the Preferred Embodiments

Construction of a Synthetic gp120 Gene Having Codons

10 Found in Highly Expressed Human Genes

A codon frequency table for the envelope precursor of the LAV subtype of HIV-1 was generated using software developed by the University of Wisconsin Genetics Computer Group. The results of that tabulation are 15 contrasted in Table 1 with the pattern of codon usage by a collection of highly expressed human genes. For any amino acid encoded by degenerate codons, the most favored codon of the highly expressed genes is different from the most favored codon of the HIV envelope precursor. 20 Moreover a simple rule describes the pattern of favored envelope codons wherever it applies: preferred codons maximize the number of adenine residues in the viral RNA. In all cases but one this means that the codon in which the third position is 25 A is the most frequently used. In the special case of serine, three codons equally contribute one A residue to the mRNA; together these three comprise 85% of the codons actually used in envelope transcripts. A particularly striking example of the A bias is found in the codon 30 choice for arginine, in which the AGA triplet comprises 88% of all codons. In addition to the preponderance of A residues, a marked preference is seen for uridine among degenerate codons whose third residue must be a pyrimidine. Finally, the inconsistencies among the less

- 9 -

frequently used variants can be accounted for by the observation that the dinucleotide CpG is underrepresented; thus the third position is less likely to be G whenever the second position is C, as in the 5 codons for alanine, proline, serine and threonine; and the CGX triplets for arginine are hardly used at all.

TABLE 1: Codon Frequency in the HIV-1 IIIb env gene and in highly expressed human genes.

		High Env				High Env			
		Cys		Gln		Glu		Gly	
		TG	C	CA	A	GA	A	GG	C
10	<u>Ala</u>	GC	C 53 T 17 A 13 G 17	27 18 50 5					
15	<u>Arg</u>	CG	C 37 T 7 A 6 G 21	0 4 0 0					
20		AG	A 10 G 18	88 8					
25	<u>Asn</u>	AA	C 78 T 22	30 70					
30	<u>Asp</u>	GA	C 75 T 25	33 67					
35	<u>Leu</u>	CT	C 26 T 5 A 3 G 58	10 7 17 17					
TT		TT	A 2 G 6	30 20					
40	<u>Lys</u>	AA	A 18 G 82	68 32					
45					<u>His</u>				
					CA	C 79 T 21	25 75		
					<u>Ile</u>	AT	C 77 T 18 A 5	25 31 44	
					<u>Ser</u>	TC	C 28 T 13 A 5	8 8 22	
						AG	C 34 T 10	22 41	
					<u>Thr</u>	AC	C 57 T 14 A 14 G 15	20 22 51 7	

- 10 -

<u>Pro</u>				<u>Tyr</u>			
CC	C	48	27	TA	C	74	8
	T	19	14		T	26	92
	A	16	55				
5	G	17	5				
<u>Phe</u>				<u>Val</u>			
TT	C	80	26	GT	C	25	12
	T	20	74		T	7	9
10					A	5	62
					G	64	18

15 Codon frequency was calculated using the GCG program established by the University of Wisconsin Genetics Computer Group. Numbers represent the percentage of cases in which the particular codon is used. Codon usage frequencies of envelope genes of other HIV-1 virus isolates are comparable and show a similar bias.

In order to produce a gp120 gene capable of high level expression in mammalian cells, a synthetic gene encoding the gp120 segment of HIV-1 was constructed (syngp120mn), based on the sequence of the most common North American subtype, HIV-1 MN (Shaw et al. 1984; Gallo et al. 1986). In this synthetic gp120 gene nearly all of the native codons have been systematically replaced with codons most frequently used in highly expressed human genes (FIG. 1). This synthetic gene was assembled from chemically synthesized oligonucleotides of 150 to 200 bases in length. If oligonucleotides exceeding 120 to 150 bases are chemically synthesized, the percentage of full-length product can be low, and the vast excess of material consists of shorter oligonucleotides. Since these shorter fragments inhibit cloning and PCR procedures, it can be very difficult to use oligonucleotides exceeding a certain length. In order to use crude synthesis material without prior purification, single-stranded oligonucleotide pools were PCR amplified before cloning. PCR products were purified in agarose gels and used as templates in the next PCR step. Two

- 11 -

adjacent fragments could be co-amplified because of overlapping sequences at the end of either fragment. These fragments, which were between 350 and 400 bp in size, were subcloned into a pCDM7-derived plasmid 5 containing the leader sequence of the CD5 surface molecule followed by a NheI/PstI/MluI/EcoR1/BamH1 polylinker. Each of the restriction enzymes in this polylinker represents a site that is present at either the 5' or 3' end of the PCR-generated fragments. Thus, 10 by sequential subcloning of each of the 4 long fragments, the whole gp120 gene was assembled. For each fragment 3 to 6 different clones were subcloned and sequenced prior to assembly. A schematic drawing of the method used to construct the synthetic gp120 is shown in FIG. 2. The 15 sequence of the synthetic gp120 gene (and a synthetic gp160 gene created using the same approach) is presented in FIG. 1.

The mutation rate was considerable. The most commonly found mutations were short (1 nucleotide) and 20 long (up to 30 nucleotides) deletions. In some cases it was necessary to exchange parts with either synthetic adapters or pieces from other subclones without mutation in that particular region. Some deviations from strict adherence to optimized codon usage were made to 25 accommodate the introduction of restriction sites into the resulting gene to facilitate the replacement of various segments (FIG. 2). These unique restriction sites were introduced into the gene at approximately 100 bp intervals. The native HIV leader sequence was exchanged 30 with the highly efficient leader peptide of the human CD5 antigen to facilitate secretion. The plasmid used for construction is a derivative of the mammalian expression vector pCDM7 transcribing the inserted gene under the control of a strong human CMV immediate early promoter.

- 12 -

To compare the wild-type and synthetic gp120 coding sequences, the synthetic gp120 coding sequence was inserted into a mammalian expression vector and tested in transient transfection assays. Several different native 5 gp120 genes were used as controls to exclude variations in expression levels between different virus isolates and artifacts induced by distinct leader sequences. The gp120 HIV IIIb construct used as control was generated by PCR using a SalI/Xhol HIV-1 HXB2 envelope fragment as 10 template. To exclude PCR induced mutations a KpnI/EarI fragment containing approximately 1.2 kb of the gene was exchanged with the respective sequence from the proviral clone. The wildtype gp120mn constructs used as controls were cloned by PCR from HIV-1 MN infected C8166 cells 15 (AIDS Repository, Rockville, MD) and expressed gp120 either with a native envelope or a CD5 leader sequence. Since proviral clones were not available in this case, two clones of each construct were tested to avoid PCR artifacts. To determine the amount of secreted gp120 20 semi-quantitatively supernatants of 293T cells transiently transfected by calcium phosphate coprecipitation were immunoprecipitated with soluble CD4:immunoglobulin fusion protein and protein A sepharose.

25 The results of this analysis (FIG. 3) show that the synthetic gene product is expressed at a very high level compared to that of the native gp120 controls. The molecular weight of the synthetic gp120 gene was comparable to control proteins (FIG. 3) and appeared to 30 be in the range of 100 to 110 kd. The slightly faster migration can be explained by the fact that in some tumor cell lines like 293T glycosylation is either not complete or altered to some extent.

To compare expression more accurately gp120 35 protein levels were quantitated using a gp120 ELISA with

- 13 -

CD4 in the demobilized phase. This analysis shows (FIG. 4) that ELISA data were comparable to the immunoprecipitation data, with a gp120 concentration of approximately 125 ng/ml for the synthetic gp120 gene, and 5 less than the background cutoff (5 ng/ml) for all the native gp120 genes. Thus, expression of the synthetic gp120 gene appears to be at least one order of magnitude higher than wildtype gp120 genes. In the experiment shown the increase was at least 25 fold.

10 The Role of rev in gp120 Expression

Since rev appears to exert its effect at several steps in the expression of a viral transcript, the possible role of non-translational effects in the improved expression of the synthetic gp120 gene was 15 tested. First, to rule out the possibility that negative signals elements conferring either increased mRNA degradation or nucleic retention were eliminated by changing the nucleotide sequence, cytoplasmic mRNA levels were tested. Cytoplasmic RNA was prepared by NP40 lysis 20 of transiently transfected 293T cells and subsequent elimination of the nuclei by centrifugation. Cytoplasmic RNA was subsequently prepared from lysates by multiple phenol extractions and precipitation, spotted on nitrocellulose using a slot blot apparatus, and finally 25 hybridized with an envelope-specific probe.

Briefly, cytoplasmic mRNA 293 cells transfected with CDM&, gp120 IIIB, or syngp120 was isolated 36 hours post transfection. Cytoplasmic RNA of Hela cells infected with wildtype vaccinia virus or recombinant 30 virus expressing gp120 IIIb or the synthetic gp120 gene was under the control of the 7.5 promoter was isolated 16 hours post infection. Equal amounts were spotted on nitrocellulose using a slot blot device and hybridized with randomly labelled 1.5 kb gp120IIIb and syngp120 35 fragments or human beta-actin. RNA expression levels

- 14 -

were quantitated by scanning the hybridized membranes with a phosphoimager. The procedures used are described in greater detail below.

This experiment demonstrated that there was no
5 significant difference in the mRNA levels of cells transfected with either the native or synthetic gp120 gene. In fact, in some experiments cytoplasmic mRNA level of the synthetic gp120 gene was even lower than that of the native gp120 gene.

10 These data were confirmed by measuring expression from recombinant vaccinia viruses. Human 293 cells or HeLa cells were infected with vaccinia virus expressing wildtype gp120 IIIb or syngp120mn at a multiplicity of infection of at least 10. Supernatants were harvested 24
15 hours post infection and immunoprecipitated with CD4:immunoglobulin fusion protein and protein A sepharose. The procedures used in this experiment are described in greater detail below.

This experiment showed that the increased
20 expression of the synthetic gene was still observed when the endogenous gene product and the synthetic gene product were expressed from vaccinia virus recombinants under the control of the strong mixed early and late 7.5k promoter. Because vaccinia virus mRNAs are transcribed
25 and translated in the cytoplasm, increased expression of the synthetic envelope gene in this experiment cannot be attributed to improved export from the nucleus. This experiment was repeated in two additional human cell types, the kidney cancer cell line 293 and HeLa cells.
30 As with transfected 293T cells, mRNA levels were similar in 293 cells infected with either recombinant vaccinia virus.

- 15 -

Codon Usage in Lentivirus

Because it appears that codon usage has a significant impact on expression in mammalian cells, the codon frequency in the envelope genes of other 5 retroviruses was examined. This study found no clear pattern of codon preference between retroviruses in general. However, if viruses from the lentivirus genus, to which HIV-1 belongs to, were analyzed separately, codon usage bias almost identical to that of HIV-1 was 10 found. A codon frequency table from the envelope glycoproteins of a variety of (predominantly type C) retroviruses excluding the lentiviruses was prepared, and compared a codon frequency table created from the envelope sequences of four lentiviruses not closely 15 related to HIV-1 (caprine arthritis encephalitis virus, equine infectious anemia virus, feline immunodeficiency virus, and visna virus) (Table 2). The codon usage pattern for lentiviruses is strikingly similar to that of HIV-1, in all cases but one, the preferred codon for 20 HIV-1 is the same as the preferred codon for the other lentiviruses. The exception is proline, which is encoded by CCT in 41% of non-HIV lentiviral envelope residues, and by CCA in 40% of residues, a situation which clearly also reflects a significant preference for the triplet 25 ending in A. The pattern of codon usage by the non-lentiviral envelope proteins does not show a similar predominance of A residues, and is also not as skewed toward third position C and G residues as is the codon usage for the highly expressed human genes. In general 30 non-lentiviral retroviruses appear to exploit the different codons more equally, a pattern they share with less highly expressed human genes.

- 16 -

TABLE 2: Codon frequency in the envelope gene of lentiviruses (lenti) and non-lentiviral retroviruses (other).

		Other Lenti				Other Lenti			
5	<u>Ala</u>	C	45	13		<u>Cys</u>	TG	53	21
	GC	T	26	37		T		47	79
		A	20	46					
		G	9	3					
10	<u>Arg</u>	C	14	2		<u>Gln</u>	CA	52	69
	CG	T	6	3			G	48	31
		A	16	5		<u>Glu</u>	GA	57	68
15		G	17	3			G	43	32
	<u>Asn</u>	A	31	51		<u>Gly</u>	GG	21	8
20	<u>AA</u>	G	15	26			C	13	9
		C	49	31			A	37	56
		T	51	69			G	29	26
	<u>Asp</u>					<u>His</u>	CA	51	38
	<u>GA</u>	C	55	33			T	49	62
		T	51	69					
25						<u>Ile</u>	AT	38	16
							C	31	22
							T	31	61
							A		
30	<u>Leu</u>	C	22	8		<u>Ser</u>	TC	38	10
	CT	T	14	9			T	17	16
		A	21	16			A	18	24
		G	19	11			G	6	5
	<u>TT</u>	A	15	41		<u>AG</u>	C	13	20
35		G	10	16			T	7	25
	<u>Lys</u>					<u>Thr</u>	AC	44	18
	<u>AA</u>	A	60	63			T	27	20
		G	40	37			A	19	55
40	<u>Pro</u>						G	10	8
	<u>CC</u>	C	42	14		<u>Tyr</u>	TA	48	28
		T	30	41			C	52	72
		A	20	40			T		
		G	7	5					

- 17 -

<u>Phe</u>				<u>Val</u>			
TT	C	52	25	GT	C	36	9
T	T	48	75	T	A	22	54
5					G	25	27

- Codon frequency was calculated using the GCG program established by the University of Wisconsin Genetics Computer Group. Numbers represent the percentage in which a particular codon is used. Codon usage of non-lentiviral retroviruses was compiled from the envelope precursor sequences of bovine leukemia virus feline leukemia virus, human T-cell leukemia virus type I, human T-cell lymphotropic virus type II, the mink cell focus-forming isolate of murine leukemia virus (MuLV), the Rauscher spleen focus-forming isolate, the 10A1 isolate, the 4070A amphotropic isolate and the myeloproliferative leukemia virus isolate, and from rat leukemia virus, simian sarcoma virus, simian T-cell leukemia virus, leukemogenic retrovirus T1223/B and gibbon ape leukemia virus. The codon frequency tables for the non-HIV, non-SIV lentiviruses were compiled from the envelope precursor sequences for caprine arthritis encephalitis virus, equine infectious anemia virus, feline immunodeficiency virus, and visna virus.

- In addition to the prevalence of A containing codons, lentiviral codons adhere to the HIV pattern of strong CpG underrepresentation, so that the third position for alanine, proline, serine and threonine triplets is rarely G. The retroviral envelope triplets show a similar, but less pronounced, underrepresentation of CpG. The most obvious difference between lentiviruses and other retroviruses with respect to CpG prevalence lies in the usage of the CGX variant of arginine triplets, which is reasonably frequently represented among the retroviral envelope coding sequences, but is almost never present among the comparable lentivirus sequences.
- 40 Differences in rev Dependence Between Native and Synthetic gp120

To examine whether regulation by rev is connected to HIV-1 codon usage, the influence of rev on the

- 18 -

expression of both native and synthetic gene was investigated. Since regulation by rev requires the rev-binding site RRE in cis, constructs were made in which this binding site was cloned into the 3' untranslated 5 region of both the native and the synthetic gene. These plasmids were co-transfected with rev or a control plasmid in trans into 293T cells, and gp120 expression levels in supernatants were measured semiquantitatively by immunoprecipitation. The procedures used in this 10 experiment are described in greater detail below.

As shown in FIG. 5, panels A and B, rev upregulates the native gp120 gene, but has no effect on the expression of the synthetic gp120 gene. Thus, the action of rev is not apparent on a substrate which lacks 15 the coding sequence of endogenous viral envelope sequences.

Expression of a synthetic rat THY-1 gene with HIV envelope codons

The above-described experiment suggest that in 20 fact "envelope sequences" have to be present for rev regulation. In order to test this hypothesis, a synthetic version of the gene encoding the small, typically highly expressed cell surface protein, rat THY-1 antigen, was prepared. The synthetic version of 25 the rat THY-1 gene was designed to have a codon usage like that of HIV gp120. In designing this synthetic gene AUUUA sequences, which are associated with mRNA instability, were avoided. In addition, two restriction sites were introduced to simplify manipulation of the 30 resulting gene (FIG. 6). This synthetic gene with the HIV envelope codon usage (rTHY-1env) was generated using three 150 to 170 mer oligonucleotides (FIG. 7). In contrast to the syngp120mn gene, PCR products were directly cloned and assembled in pUC12, and subsequently 35 cloned into pCDM7.

- 19 -

Expression levels of native rTHY-1 and rTHY-1 with the HIV envelope codons were quantitated by immunofluorescence of transiently transfected 293T cells. FIG 8 shows that the expression of the native THY-1 gene 5 is almost two orders of magnitude above the background level of the control transfected cells (pCDM7). In contrast, expression of the synthetic rat THY-1 is substantially lower than that of the native gene (shown by the shift to of the peak towards a lower channel 10 number).

To prove that no negative sequence elements promoting mRNA degradation were inadvertently introduced, a construct was generated in which the rTHY-1env gene was cloned at the 3' end of the synthetic gp120 gene (FIG. 9, 15 panel B). In this experiment 293T cells were transfected with either the syngp120mn gene or the syngp120/rat THY-1 env fusion gene (syngp120mn.rTHY-1env). Expression was measured by immunoprecipitation with CD4:IgG fusion protein and protein A agarose. The procedures used in 20 this experiment are described in greater detail below.

Since the synthetic gp120 gene has an UAG stop codon, rTHY-1env is not translated from this transcript. If negative elements conferring enhanced degradation were present in the sequence, gp120 protein levels expressed 25 from this construct should be decreased in comparison to the syngp120mn construct without rTHY-1env. FIG. 9, panel A, shows that the expression of both constructs is similar, indicating that the low expression must be linked to translation.

30 Rev-dependent expression of synthetic rat THY-1 gene with envelope codons

To explore whether rev is able to regulate expression of a rat THY-1 gene having env codons, a construct was made with a rev-binding site in the 3' end 35 of the rTHY1env open reading frame. To measure rev-

- 20 -

responsiveness of the a rat THY-1env construct having a 3' RRE, human 293T cells were cotransfected ratTHY-1envrre and either CDM7 or pCMVrev. At 60 hours post transfection cells were detached with 1 mM EDTA in 5 PBS and stained with the OX-7 anti rTHY-1 mouse monoclonal antibody and a secondary FITC-conjugated antibody. Fluorescence intensity was measured using a EPICS XL cytofluorometer. These procedures are described in greater detail below.

10 In repeated experiments, a slight increase of rTHY-1env expression was detected if rev was cotransfected with the rTHY-1env gene. To further increase the sensitivity of the assay system a construct expressing a secreted version of rTHY-1env was generated. 15 This construct should produce more reliable data because the accumulated amount of secreted protein in the supernatant reflects the result of protein production over an extended period, in contrast to surface expressed protein, which appears to more closely reflect the 20 current production rate. A gene capable of expressing a secreted form was prepared by PCR using forward and reverse primers annealing 3' of the endogenous leader sequence and 5' of the sequence motif required for phosphatidylinositol glycan anchorage respectively. The 25 PCR product was cloned into a plasmid which already contained a CD5 leader sequence, thus generating a construct in which the membrane anchor has been deleted and the leader sequence exchanged by a heterologous (and probably more efficient) leader peptide.

30 The rev-responsiveness of the secreted form ratTHY-1env was measured by immunoprecipitation of supernatants of human 293T cells cotransfected with a plasmid expressing a secreted form of ratTHY-1env and the RRE sequence in cis (rTHY-1envPI-rre) and either CDM7 or 35 pCMVrev. The rTHY-1envPI-RRE construct was made by PCR

- 21 -

using the oligonucleotides
cgcggggctagcgcaaagagtaataagtttaac as forward and
cgcggatcccttgtatttgtactaata as reverse primers and the
synthetic rTHY-1env construct as template. After
5 digestion with NheI and NotI the PCR fragment was cloned
into a plasmid containing CD5 leader and RRE sequences.
Supernatants of ³⁵S labelled cells were harvested 72
hours post transfection, precipitated with a mouse
monoclonal antibody OX7 against rTHY-1 and anti mouse IgG
10 sepharose, and run on a 12% reducing SDS-PAGE.

In this experiment the induction of rTHY-1env by
rev was much more prominent and clearcut than in the
above-described experiment and strongly suggests that rev
is able to translationally regulate transcripts that are
15 suppressed by low-usage codons.

Rev-independent expression of a rTHY-1env:immunoglobulin fusion protein

To test whether low-usage codons must be present
throughout the whole coding sequence or whether a short
20 region is sufficient to confer rev-responsiveness, a
rTHY-1env:immunoglobulin fusion protein was generated.
In this construct the rTHY-1env gene (without the
sequence motif responsible for phosphatidylinositol
glycan anchorage) is linked to the human IgG1 hinge, CH2
25 and CH3 domains. This construct was generated by anchor
PCR using primers with NheI and BamHI restriction sites
and rTHY-1env as template. The PCR fragment was cloned
into a plasmid containing the leader sequence of the CD5
surface molecule and the hinge, CH2 and CH3 parts of
30 human IgG1 immunoglobulin. A Hind3/Eag1 fragment
containing the rTHY-1envgen insert was subsequently
cloned into a pCDM7-derived plasmid with the RRE
sequence.

To measure the response of the rTHY-1env/
35 immunoglobulin fusion gene (rTHY-1envgenRRE) to rev human
293T cells cotransfected with rTHY-1envgenRRE and either

- 22 -

pCDM7 or pCMVrev. The rTHY-1enveg1rre construct was made by anchor PCR using forward and reverse primers with NheI and BamH1 restriction sites respectively. The PCR fragment was cloned into a plasmid containing a CD5 leader and human IgG1 hinge, CH2 and CH3 domains.

Supernatants of ³⁵S labelled cells were harvested 72 hours post transfection, precipitated with a mouse monoclonal antibody OX7 against rTHY-1 and anti mouse IgG sepharose, and run on a 12% reducing SDS-PAGE. The procedures used are described in greater detail below.

As with the product of the rTHY-1envPI- gene, this rTHY-1env/immunoglobulin fusion protein is secreted into the supernatant. Thus, this gene should be responsive to rev-induction. However, in contrast to rTHY-1envPI-, cotransfection of rev in trans induced no or only a negligible increase of rTHY-1enveg1 expression.

The expression of rTHY-1:immunoglobulin fusion protein with native rTHY-1 or HIV envelope codons was measured by immunoprecipitation. Briefly, human 293T cells transfected with either rTHY-1enveg1 (env codons) or rTHY-1wteg1 (native codons). The rTHY-1wteg1 construct was generated in manner similar to that used for the rTHY-1enveg1 construct, with the exception that a plasmid containing the native rTHY-1 gene was used as template. Supernatants of ³⁵S labelled cells were harvested 72 hours post transfection, precipitated with a mouse monoclonal antibody OX7 against rTHY-1 and anti mouse IgG sepharose, and run on a 12% reducing SDS-PAGE. The procedures used in this experiment are described in greater detail below.

Expression levels of rTHY-1enveg1 were decreased in comparison to a similar construct with wildtype rTHY-1 as the fusion partner, but were still considerably higher than rTHY-1env. Accordingly, both parts of the fusion protein influenced expression levels. The addition of

- 23 -

rTHY-1env did not restrict expression to an equal level as seen for rTHY-1env alone. Thus, regulation by rev appears to be ineffective if protein expression is not almost completely suppressed.

5 Codon preference in HIV-1 envelope genes

Direct comparison between codon usage frequency of HIV envelope and highly expressed human genes reveals a striking difference for all twenty amino acids. One simple measure of the statistical significance of this 10 codon preference is the finding that among the nine amino acids with two fold codon degeneracy, the favored third residue is A or U in all nine. The probability that all nine of two equiprobable choices will be the same is approximately 0.004, and hence by any conventional 15 measure the third residue choice cannot be considered random. Further evidence of a skewed codon preference is found among the more degenerate codons, where a strong selection for triplets bearing adenine can be seen. This contrasts with the pattern for highly expressed genes, 20 which favor codons bearing C, or less commonly G, in the third position of codons with three or more fold degeneracy.

The systematic exchange of native codons with codons of highly expressed human genes dramatically 25 increased expression of gp120. A quantitative analysis by ELISA showed that expression of the synthetic gene was at least 25 fold higher in comparison to native gp120 after transient transfection into human 293 cells. The concentration levels in the ELISA experiment shown were 30 rather low. Since an ELISA was used for quantification which is based on gp120 binding to CD4, only native, non-denatured material was detected. This may explain the apparent low expression. Measurement of cytoplasmic mRNA levels demonstrated that the difference in protein

- 24 -

expression is due to translational differences and not mRNA stability.

Retroviruses in general do not show a similar preference towards A and T as found for HIV. But if this family was divided into two subgroups, lentiviruses and non-lentiviral retroviruses, a similar preference to A and, less frequently, T, was detected at the third codon position for lentiviruses. Thus, the availing evidence suggests that lentiviruses retain a characteristic pattern of envelope codons not because of an inherent advantage to the reverse transcription or replication of such residues, but rather for some reason peculiar to the physiology of that class of viruses. The major difference between lentiviruses and non-complex retroviruses are additional regulatory and non-essentially accessory genes in lentiviruses, as already mentioned. Thus, one simple explanation for the restriction of envelope expression might be that an important regulatory mechanism of one of these additional molecules is based on it. In fact, it is known that one of these proteins, rev, which most likely has homologues in all lentiviruses. Thus codon usage in viral mRNA is used to create a class of transcripts which is susceptible to the stimulatory action of rev. This hypothesis was proved using a similar strategy as above, but this time codon usage was changed into the inverse direction. Codon usage of a highly expressed cellular gene was substituted with the most frequently used codons in the HIV envelope. As assumed, expression levels were considerably lower in comparison to the native molecule, almost two orders of magnitude when analyzed by immunofluorescence of the surface expressed molecule (see 4.7). If rev was coexpressed in trans and a RRE element was present in cis only a slight induction was found for the surface molecule. However, if THY-1 was expressed as

- 25 -

a secreted molecule, the induction by rev was much more prominent, supporting the above hypothesis. This can probably be explained by accumulation of secreted protein in the supernatant, which considerably amplifies the rev effect. If rev only induces a minor increase for surface molecules in general, induction of HIV envelope by rev cannot have the purpose of an increased surface abundance, but rather of an increased intracellular gp160 level. It is completely unclear at the moment why this 10 should be the case.

To test whether small subtotal elements of a gene are sufficient to restrict expression and render it rev-dependent rTHY1env:immunoglobulin fusion proteins were generated, in which only about one third of the total 15 gene had the envelope codon usage. Expression levels of this construct were on an intermediate level, indicating that the rTHY-1env negative sequence element is not dominant over the immunoglobulin part. This fusion protein was not or only slightly rev-responsive, 20 indicating that only genes almost completely suppressed can be rev-responsive.

Another characteristic feature that was found in the codon frequency tables is a striking underrepresentation of CpG triplets. In a comparative 25 study of codon usage in E. coli, yeast, drosophila and primates it was shown that in a high number of analyzed primate genes the 8 least used codons contain all codons with the CpG dinucleotide sequence. Avoidance of codons containing this dinucleotide motif was also found in the 30 sequence of other retroviruses. It seems plausible that the reason for underrepresentation of CpG-bearing triplets has something to do with avoidance of gene silencing by methylation of CpG cytosines. The expected number of CpG dinucleotides for HIV as a whole is about 35 one fifth that expected on the basis of the base

- 26 -

composition. This might indicate that the possibility of high expression is restored, and that the gene in fact has to be highly expressed at some point during viral pathogenesis.

5 The results presented herein clearly indicate that codon preference has a severe effect on protein levels, and suggest that translational elongation is controlling mammalian gene expression. However, other factors may play a role. First, abundance of not maximally loaded
10 mRNA's in eukaryotic cells indicates that initiation is rate limiting for translation in at least some cases, since otherwise all transcripts would be completely covered by ribosomes. Furthermore, if ribosome stalling and subsequent mRNA degradation were the mechanism,
15 suppression by rare codons could most likely not be reversed by any regulatory mechanism like the one presented herein. One possible explanation for the influence of both initiation and elongation on translational activity is that the rate of initiation, or
20 access to ribosomes, is controlled in part by cues distributed throughout the RNA, such that the lentiviral codons predispose the RNA to accumulate in a pool of poorly initiated RNAs. However, this limitation need not be kinetic; for example, the choice of codons could
25 influence the probability that a given translation product, once initiated, is properly completed. Under this mechanism, abundance of less favored codons would incur a significant cumulative probability of failure to complete the nascent polypeptide chain. The sequestered
30 RNA would then be lent an improved rate of initiation by the action of rev. Since adenine residues are abundant in rev-responsive transcripts, it could be that RNA adenine methylation mediates this translational suppression.

- 27 -

Detailed Procedures

The following procedures were used in the above-described experiments.

Sequence Analysis

5 Sequence analyses employed the software developed by the University of Wisconsin Computer Group.

Plasmid constructions

Plasmid constructions employed the following methods. Vectors and insert DNA was digested at a 10 concentration of 0.5 μ g/10 μ l in the appropriate restriction buffer for 1 - 4 hours (total reaction volume approximately 30 μ l). Digested vector was treated with 10% (v/v) of 1 μ g/ml calf intestine alkaline phosphatase for 30 min prior to gel electrophoresis. Both vector and 15 insert digests (5 to 10 μ l each) were run on a 1.5% low melting agarose gel with TAE buffer. Gel slices containing bands of interest were transferred into a 1.5 ml reaction tube, melted at 65°C and directly added to the ligation without removal of the agarose. Ligations 20 were typically done in a total volume of 25 μ l in 1x Low Buffer 1x Ligation Additions with 200-400 U of ligase, 1 μ l of vector, and 4 μ l of insert. When necessary, 5' overhanging ends were filled by adding 1/10 volume of 250 μ M dNTPs and 2-5 U of Klenow polymerase to heat 25 inactivated or phenol extracted digests and incubating for approximately 20 min at room temperature. When necessary, 3' overhanging ends were filled by adding 1/10 volume of 2.5 mM dNTPs and 5-10 U of T4 DNA polymerase to heat inactivated or phenol extracted digests, followed by 30 incubation at 37°C for 30 min. The following buffers were used in these reactions: 10x Low buffer (60 mM Tris HCl, pH 7.5, 60 mM MgCl₂, 50 mM NaCl, 4 mg/ml BSA, 70 mM β -mercaptoethanol, 0.02% NaN₃); 10x Medium buffer (60 mM Tris HCl, pH 7.5, 60 mM MgCl₂, 50 mM NaCl, 4 mg/ml BSA, 35 70 mM β -mercaptoethanol, 0.02% NaN₃); 10x High buffer (60

- 28 -

mM Tris HCl, pH 7.5, 60 mM MgCl₂, 50 mM NaCl, 4 mg/ml BSA, 70 mM β-mercaptoethanol, 0.02% NaN₃); 10x Ligation additions (1 mM ATP, 20 mM DTT, 1 mg/ml BSA, 10 mM spermidine); 50x TAE (2 M Tris acetate, 50 mM EDTA).

5 Oligonucleotide synthesis and purification

Oligonucleotides were produced on a Milligen 8750 synthesizer (Millipore). The columns were eluted with 1 ml of 30% ammonium hydroxide, and the eluted oligonucleotides were deblocked at 55°C for 6 to 12 hours. After deblocking, 150 μl of oligonucleotide were precipitated with 10x volume of unsaturated n-butanol in 1.5 ml reaction tubes, followed by centrifugation at 15,000 rpm in a microfuge. The pellet was washed with 70% ethanol and resuspended in 50 μl of H₂O. The concentration was determined by measuring the optical density at 260 nm in a dilution of 1:333 (1 OD₂₆₀ = 30 μg/ml).

The following oligonucleotides were used for construction of the synthetic gp120 gene (all sequences shown in this text are in 5' to 3' direction).

oligo 1 forward (NheI): cgc ggg cta gcc acc gag aag ctg (SEQ ID NO: 1).

oligo 1: acc gag aag ctg tgg gtg acc gtg tac tac ggc gtg ccc gtg tgg aag ag ag gcc acc acc acc ctg ttc tgc 25 gcc agc gac gcc aag gcg tac gac acc gag gtg cac aac gtg tgg gcc acc cag gcg tgc gtg ccc acc gac ccc aac ccc cag gag gtg gag ctc gtg aacgtg acc gag aac ttc aac atg (SEQ ID NO: 2).

oligo 1 reverse: cca cca tgt tgt tct tcc aca tgt 30 tga agt tct c (SEQ ID NO: 3).

oligo 2 forward: gac cga gaa ctt caa cat gtg gaa gaa caa cat (SEQ ID NO: 4)

oligo 2: tgg aag aac aac atg gtg gag cag atg cat gag gac atc atc agc ctg tgg gac cag agc ctg aag ccc tgc 35 gtg aag ctg acc cc ctg tgc gtg acc tg aac tgc acc gac ctg

- 29 -

agg aac acc acc aac acc aac ac agc acc gcc aac aac aac
agc aac agc gag ggc acc atc aag ggc ggc gag atg (SEQ ID
NO: 5).

oligo 2 reverse (PstI): gtt gaa gct gca gtt ctt
5 cat ctc gcc gcc ctt (SEQ ID NO: 6).

oligo 3 forward (PstI): gaa gaa ctg cag ctt caa
cat cac cac cag c (SEQ ID NO: 7).

oligo 3: aac atc acc acc agc atc cgc gac aag atg
cag aag gag tac gcc ctg ctg tac aag ctg gat atc gtg agc
10 atc gac aac gac agc acc agc tac cgc ctg atc tcc tgc
aac acc agc gtg atc acc cag gcc tgc ccc aag atc agc ttc
gag ccc atc ccc atc cac tac tgc gcc ccc gcc ggc ttc gcc
(SEQ ID NO: 8).

oligo 3 reverse: gaa ctt ctt gtc ggc ggc gaa gcc
15 ggc ggg (SEQ ID NO: 9).

oligo 4 forward: gcg ccc ccg ccg gct tcg cca tcc
tga agt gca acg aca aga agt tc (SEQ ID NO: 10)

oligo 4: gcc gac aag aag ttc agc ggc aag ggc agc
tgc aag aac gtg agc acc gtg cag tgc acc cac ggc atc cgg
20 ccg gtg gtg agc acc cag ctc ctg ctg aac ggc agc ctg gcc
gag gag gag gtg gtg atc cgc agc gag aac ttc acc gac aac
gcc aag acc atc atc gtg cac ctg aat gag agc gtg cag atc
(SEQ ID NO: 11)

oligo 4 reverse (MluI): agt tgg gac gcg tgc agt
25 tga tct gca cgc tct c (SEQ ID NO: 12).

oligo 5 forward (MluI): gag agc gtg cag atc aac
tgc acg cgt ccc (SEQ ID NO: 13).

oligo 5: aac tgc acg cgt ccc aac tac aac aag cgc
aag cgc atc cac atc ggc ccc ggg cgc gcc ttc tac acc acc
30 aag aac atc atc ggc acc atc ctc cag gcc cac tgc aac atc
tct aga (SEQ ID NO: 14) .

oligo 5 reverse: gtc gtt cca ctt ggc tct aga gat
gtt gca (SEQ ID NO: 15).

oligo 6 forward: gca aca tct cta gag cca agt gga
35 acg ac (SEQ ID NO: 16).

- 30 -

oligo 6: gcc aag tgg aac gac acc ctg cgc cag atc
gtg agc aag ctg aag gag cag ttc aag aac aag acc atc gtg
ttc ac cag agc agc ggc ggc gac ccc gag atc gtg atg cac
agc ttc aac tgc ggc ggc (SEQ ID NO: 17).

5 oligo 6 reverse (EcoR1): gca gta gaa gaa ttc gcc
gcc gca gtt ga (SEQ ID NO: 18).

oligo 7 forward (EcoR1): tca act gcg gcg gcg aat
tct tct act gc (SEQ ID NO: 19).

oligo 7: ggc gaa ttc ttc tac tgc aac acc agc ccc
10 ctg ttc aac agc acc tgg aac ggc aac aac acc tgg aac aac
acc acc ggc agc aac aac aat att acc ctc cag tgc aag atc
aag cag atc atc aac atg tgg cag gag gtg ggc aag gcc atg
tat gcc ccc ccc atc gag ggc cag atc cgg tgc agc agc (SEQ
ID NO: 20)

15 oligo 7 reverse: gca gac cgg tga tgt tgc tgc tgc
acc gga tct ggc cct c (SEQ ID NO: 21).

oligo 8 forward: cga ggg cca gat ccg gtg cag cag
caa cat cac cgg tct g (SEQ ID NO: 22).

oligo 8: aac atc acc ggt ctg ctg ctg acc cgc gac
20 ggc ggc aag gac acc gac acc aac gac acc gaa atc ttc cgc
ccc ggc ggc gac atg cgc gac aac tgg aga tct gag ctg
tac aag tac aag gtg gtg acg atc gag ccc ctg ggc gtg gcc
ccc acc aag gcc aag cgc cgc gtg gtg cag cgc gag aag cgc
(SEQ ID NO: 23).

25 oligo 8 reverse (Not1): cgc ggg cgg ccg ctt tag
cgc ttc tcg cgc tgc acc ac (SEQ ID NO: 24).

The following oligonucleotides were used for the
construction of the ratTHY-1env gene.

oligo 1 forward (BamH1/Hind3): cgc ggg gga tcc
30 aag ctt acc atg att cca gta ata agt (SEQ ID NO: 25).

oligo 1: atg aat cca gta ata agt ata aca tta tta
tta agt gta tta caa atg agt aga gga caa aga gta ata agt
tta aca gca tct tta gta aat caa aat ttg aga tta gat tgt
aga cat gaa aat aat aca aat ttg cca ata caa cat gaa ttt
35 tca tta acg (SEQ ID NO: 26).

- 31 -

oligo 1 reverse (EcoR1/Mlu1): cgc ggg gaa ttc acg
cgt taa tga aaa ttc atg ttg (SEQ ID NO: 27).

oligo 2 forward (BamH1/Mlu1): cgc gga tcc acg cgt
gaa aaa aaa aaa cat (SEQ ID NO: 28).

5 oligo 2: cgt gaa aaa aaa aaa cat gta tta agt gga
aca tta gga gta cca gaa cat aca tat aga agt aga gta aat
ttg ttt agt gat aga ttc ata aaa gta tta aca tta gca aat
ttt aca aca aaa gat gaa gga gat tat atg tgt gag (SEQ ID
NO: 29).

10 oligo 2 reverse (EcoR1/Sac1): cgc gaa ttc gag ctc
aca cat ata atc tcc (SEQ ID NO: 30).

oligo 3 forward (BamH1/Sac1): cgc gga tcc gag ctc
aga gta agt gga caa (SEQ ID NO: 31).

15 oligo 3: ctc aga gta agt gga caa aat cca aca agt
agt aat aaa aca ata aat gta ata aga gat aaa tta gta aaa
tgt ga gga ata agt tta tta gta caa aat aca agt tgg tta
tta tta tta tta agt tta agt ttt tta caa gca aca gat
ttt ata agt tta tga (SEQ ID NO: 32).

20 oligo 3 reverse (EcoR1/Not1): cgc gaa ttc gcg gcc
gct tca taa act tat aaa atc (SEQ ID NO: 33).

Polymerase Chain Reaction

Short, overlapping 15 to 25 mer oligonucleotides annealing at both ends were used to amplify the long oligonucleotides by polymerase chain reaction (PCR).

25 Typical PCR conditions were: 35 cycles, 55°C annealing temperature, 0.2 sec extension time. PCR products were gel purified, phenol extracted, and used in a subsequent PCR to generate longer fragments consisting of two adjacent small fragments. These longer fragments were
30 cloned into a CDM7-derived plasmid containing a leader sequence of the CD5 surface molecule followed by a NheI/PstI/MluI/EcoR1/BamH1 polylinker.

The following solutions were used in these reactions: 10x PCR buffer (500 mM KCl, 100 mM Tris HCl, pH 7.5, 8 mM MgCl₂, 2 mM each dNTP). The final buffer

- 32 -

was complemented with 10% DMSO to increase fidelity of the Taq polymerase.

Small scale DNA preparation

Transformed bacteria were grown in 3 ml LB
5 cultures for more than 6 hours or overnight.
Approximately 1.5 ml of each culture was poured into 1.5
ml microfuge tubes, spun for 20 seconds to pellet cells
and resuspended in 200 μ l of solution I. Subsequently
400 μ l of solution II and 300 μ l of solution III were
10 added. The microfuge tubes were capped, mixed and spun
for > 30 sec. Supernatants were transferred into fresh
tubes and phenol extracted once. DNA was precipitated by
filling the tubes with isopropanol, mixing, and spinning
in a microfuge for > 2 min. The pellets were rinsed in
15 70 % ethanol and resuspended in 50 μ l dH₂O containing 10
 μ l of RNase A. The following media and solutions were
used in these procedures: LB medium (1.0 % NaCl, 0.5%
yeast extract, 1.0% tryptone); solution I (10 mM EDTA pH
8.0); solution II (0.2 M NaOH, 1.0% SDS); solution III
20 (2.5 M KOAc, 2.5 M glacial acetic acid); phenol (pH
adjusted to 6.0, overlaid with TE); TE (10 mM Tris HCl,
pH 7.5, 1 mM EDTA pH 8.0).

Large scale DNA preparation

One liter cultures of transformed bacteria were
25 grown 24 to 36 hours (MC1061p3 transformed with pCDM
derivatives) or 12 to 16 hours (MC1061 transformed with
pUC derivatives) at 37°C in either M9 bacterial medium
(pCDM derivatives) or LB (pUC derivatives). Bacteria
were spun down in 1 liter bottles using a Beckman J6
30 centrifuge at 4,200 rpm for 20 min. The pellet was
resuspended in 40 ml of solution I. Subsequently, 80 ml
of solution II and 40 ml of solution III were added and
the bottles were shaken semivigorously until lumps of 2
to 3 mm size developed. The bottle was spun at 4,200 rpm
35 for 5 min and the supernatant was poured through

- 33 -

cheesecloth into a 250 ml bottle. Isopropanol was added to the top and the bottle was spun at 4,200 rpm for 10 min. The pellet was resuspended in 4.1 ml of solution I and added to 4.5 g of cesium chloride, 0.3 ml of 10 mg/ml 5 ethidium bromide, and 0.1 ml of 1% Triton X100 solution. The tubes were spun in a Beckman J2 high speed centrifuge at 10,000 rpm for 5 min. The supernatant was transferred into Beckman Quick Seal ultracentrifuge tubes, which were then sealed and spun in a Beckman ultracentrifuge using a 10 NVT90 fixed angle rotor at 80,000 rpm for > 2.5 hours. The band was extracted by visible light using a 1 ml syringe and 20 gauge needle. An equal volume of dH₂O was added to the extracted material. DNA was extracted once with n-butanol saturated with 1 M sodium chloride, 15 followed by addition of an equal volume of 10 M ammonium acetate/ 1 mM EDTA. The material was poured into a 13 ml snap tube which was then filled to the top with absolute ethanol, mixed, and spun in a Beckman J2 centrifuge at 10,000 rpm for 10 min. The pellet was rinsed with 70% 20 ethanol and resuspended in 0.5 to 1 ml of H₂O. The DNA concentration was determined by measuring the optical density at 260 nm in a dilution of 1:200 (1 OD₂₆₀ = 50 µg/ml).

The following media and buffers were used in these 25 procedures: M9 bacterial medium (10 g M9 salts, 10 g casamino acids (hydrolysed), 10 ml M9 additions, 7.5 µg/ml tetracycline (500 µl of a 15 mg/ml stock solution), 12.5 µg/ml ampicillin (125 µl of a 10 mg/ml stock solution); M9 additions (10 mM CaCl₂, 100 mM MgSO₄, 200 30 µg/ml thiamine, 70% glycerol); LB medium (1.0 % NaCl, 0.5 % yeast extract, 1.0 % tryptone); Solution I (10 mM EDTA pH 8.0); Solution II (0.2 M NaOH 1.0 % SDS); Solution III (2.5 M KOAc 2.5 M HOAc)

- 34 -

Sequencing

Synthetic genes were sequenced by the Sanger dideoxynucleotide method. In brief, 20 to 50 µg double-stranded plasmid DNA were denatured in 0.5 M NaOH for 5 min. Subsequently the DNA was precipitated with 1/10 volume of sodium acetate (pH 5.2) and 2 volumes of ethanol and centrifuged for 5 min. The pellet was washed with 70% ethanol and resuspended at a concentration of 1 µg/µl. The annealing reaction was carried out with 4 µg of template DNA and 40 ng of primer in 1x annealing buffer in a final volume of 10 µl. The reaction was heated to 65°C and slowly cooled to 37°C. In a separate tube 1 µl of 0.1 M DTT, 2 µl of labeling mix, 0.75 µl of dH₂O, 1 µl of [³⁵S] dATP (10 uCi), and 0.25 µl of 15 Sequenase™ (12 U/µl) were added for each reaction. Five µl of this mix were added to each annealed primer-template tube and incubated for 5 min at room temperature. For each labeling reaction 2.5 µl of each of the 4 termination mixes were added on a Terasaki plate 20 and prewarmed at 37°C. At the end of the incubation period 3.5 µl of labeling reaction were added to each of the 4 termination mixes. After 5 min, 4 µl of stop solution were added to each reaction and the Terasaki plate was incubated at 80°C for 10 min in an oven. The 25 sequencing reactions were run on 5% denaturing polyacrylamide gel. An acrylamide solution was prepared by adding 200 ml of 10x TBE buffer and 957 ml of dH₂O to 100 g of acrylamide:bisacrylamide (29:1). 5% polyacrylamide 46% urea and 1x TBE gel was prepared by 30 combining 38 ml of acrylamide solution and 28 g urea. Polymerization was initiated by the addition of 400 µl of 10% ammonium peroxodisulfate and 60 µl of TEMED. Gels were poured using silanized glass plates and sharktooth combs and run in 1x TBE buffer at 60 to 100 W for 2 to 4 35 hours (depending on the region to be read). Gels were

- 35 -

- transferred to Whatman blotting paper, dried at 80°C for about 1 hour, and exposed to x-ray film at room temperature. Typically exposure time was 12 hours. The following solutions were used in these procedures:
- 5 Annealing buffer (200 mM Tris HCl, pH 7.5, 100 mM MgCl₂, 250 mM NaCl); Labelling Mix (7.5 μM each dCTP, dGTP, and dTTP); Termination Mixes (80 μM each dNTP, 50 mM NaCl, 8 μM ddNTP (one each)); Stop solution (95% formamide, 20 mM EDTA, 0.05 % bromphenol blue, 0.05 % xylencyanol); 5x TBE (0.9 M Tris borate, 20 mM EDTA); Polyacrylamide solution (96.7 g polyacrylamide, 3.3 g bisacrylamide, 200 ml 1x TBE, 957 ml dH₂O).
- 10 RNA isolation

- Cytoplasmic RNA was isolated from calcium phosphate transfected 293T cells 36 hours post transfection and from vaccinia infected HeLa cells 16 hours post infection essentially as described by Gilman. (Gilman Preparation of cytoplasmic RNA from tissue culture cells. In Current Protocols in Molecular Biology, Ausubel et al, eds., Wiley & Sons, New York, 1992). Briefly, cells were lysed in 400 μl lysis buffer, nuclei were spun out, and SDS and proteinase K were added to 0.2% and 0.2 mg/ml respectively. The cytoplasmic extracts were incubated at 37°C for 20 min, 25 phenol/chloroform extracted twice, and precipitated. The RNA was dissolved in 100 μl buffer I and incubated at 37°C for 20 min. The reaction was stopped by adding 25 μl stop buffer and precipitated again.

- The following solutions were used in this procedure: Lysis Buffer (TE containing with 50 mM Tris pH 8.0, 100 mM NaCl, 5 mM MgCl₂, 0.5% NP40); Buffer I (TE buffer with 10 mM MgCl₂, 1 mM DTT, 0.5 U/μl placental RNase inhibitor, 0.1 U/μl RNase free DNase I); Stop buffer (50 mM EDTA 1.5 M NaOAc 1.0 % SDS).

- 36 -

Slot blot analysis

For slot blot analysis 10 µg of cytoplasmic RNA was dissolved in 50 µl dH₂O to which 150 µl of 10x SSC/1% formaldehyde were added. The solubilized RNA was 5 then incubated at 65°C for 15 min and spotted onto with a slot blot apparatus. Radioactively labelled probes of 1.5 kb gp120IIIb and syngp120mn fragments were used for hybridization. Each of the two fragments was random labelled in a 50 µl reaction with 10 µl of 5x oligo- 10 labelling buffer, 8 µl of 2.5 mg/ml BSA, 4 µl of α [³²P]-dCTP (20 uCi/µl; 6000 Ci/mmol), and 5 U of Klenow fragment. After 1 to 3 hours incubation at 37°C 100 µl of TE were added and unincorporated α [³²P]-dCTP was eliminated using G50 spin column. Activity was measured 15 in a Beckman beta-counter, and equal specific activities were used for hybridization. Membranes were pre-hybridized for 2 hours and hybridized for 12 to 24 hours at 42°C with 0.5 x 10⁶ cpm probe per ml hybridization fluid. The membrane was washed twice (5 min) with 20 washing buffer I at room temperature, for one hour in washing buffer II at 65°C, and then exposed to x-ray film. Similar results were obtained using a 1.1 kb NotI/SfiI fragment of pCDM7 containing the 3 untranslated region. Control hybridizations were done in parallel 25 with a random-labelled human beta-actin probe. RNA expression was quantitated by scanning the hybridized nitrocellulose membranes with a Magnetic Dynamics phosphorimager.

The following solutions were used in this
30 procedure:
5x Oligo-labelling buffer (250 mM Tris HCl, pH 8.0, 25 mM MgCl₂, 5 mM β -mercaptoethanol, 2 mM dATP, 2mM dGTP, 2mM dTTP, 1 M Hepes pH 6.6, 1 mg/ml hexanucleotides [dNTP]6);
Hybridization Solution (M sodium phosphate, 250 mM
35 NaCl, 7% SDS, 1 mM EDTA, 5% dextrane sulfate, 50%

- 37 -

formamide, 100 µg/ml denatured salmon sperm DNA); Washing buffer I (2x SSC, 0.1% SDS); Washing buffer II (0.5x SSC, 0.1% SDS); 20x SSC (3 M NaCl, 0.3 M Na₃citrate, pH adjusted to 7.0).

5 Vaccinia recombination

Vaccinia recombination used a modification of the of the method described by Romeo and Seed (Romeo and Seed, Cell, 64: 1037, 1991). Briefly, CV1 cells at 70 to 90% confluency were infected with 1 to 3 µl of a wildtype 10 vaccinia stock WR (2×10^8 pfu/ml) for 1 hour in culture medium without calf serum. After 24 hours, the cells were transfected by calcium phosphate with 25 µg TKG plasmid DNA per dish. After an additional 24 to 48 hours the cells were scraped off the plate, spun down, and 15 resuspended in a volume of 1 ml. After 3 freeze/thaw cycles trypsin was added to 0.05 mg/ml and lysates were incubated for 20 min. A dilution series of 10, 1 and 0.1 µl of this lysate was used to infect small dishes (6 cm) of CV1 cells, that had been pretreated with 12.5 µg/ml 20 mycophenolic acid, 0.25 mg/ml xanthin and 1.36 mg/ml hypoxanthine for 6 hours. Infected cells were cultured for 2 to 3 days, and subsequently stained with the monoclonal antibody NEA9301 against gp120 and an alkaline phosphatase conjugated secondary antibody. Cells were 25 incubated with 0.33 mg/ml NBT and 0.16 mg/ml BCIP in AP-buffer and finally overlaid with 1% agarose in PBS. Positive plaques were picked and resuspended in 100 µl Tris pH 9.0. The plaque purification was repeated once. To produce high titer stocks the infection was slowly 30 scaled up. Finally, one large plate of Hela cells was infected with half of the virus of the previous round. Infected cells were detached in 3 ml of PBS, lysed with a Dounce homogenizer and cleared from larger debris by centrifugation. VPE-8 recombinant vaccinia stocks were 35 kindly provided by the AIDS repository, Rockville, MD,

- 38 -

and express HIV-1 IIIB gp120 under the 7.5 mixed early/late promoter (Earl et al., J. Virol., 65:31, 1991). In all experiments with recombinant vaccinia cells were infected at a multiplicity of infection of at least 5 10.

The following solution was used in this procedure:
AP buffer (100 mM Tris HCl, pH 9.5, 100 mM NaCl, 5 mM MgCl₂)

Cell culture

10 The monkey kidney carcinoma cell lines CV1 and Cos7, the human kidney carcinoma cell line 293T, and the human cervix carcinoma cell line Hela were obtained from the American Tissue Typing Collection and were maintained in supplemented IMDM. They were kept on 10 cm tissue
15 culture plates and typically split 1:5 to 1:20 every 3 to 4 days. The following medium was used in this procedure:

Supplemented IMDM (90% Iscove's modified Dulbecco Medium, 10% calf serum, iron-complemented, heat inactivated 30
20 min 56°C, 0.3 mg/ml L-glutamine, 25 µg/ml gentamycin 0.5 mM β-mercaptoethanol (pH adjusted with 5 M NaOH, 0.5 ml)).

Transfection

Calcium phosphate transfection of 293T cells was
25 performed by slowly adding and under vortexing 10 µg plasmid DNA in 250 µl 0.25 M CaCl₂ to the same volume of 2x HEBS buffer while vortexing. After incubation for 10 to 30 min at room temperature the DNA precipitate was added to a small dish of 50 to 70% confluent cells. In
30 cotransfection experiments with rev, cells were transfected with 10 µg gp120IIIB, gp120IIIBrre, syngp120mnrre or rTHY-1envgirre and 10 µg of pCMVrev or CDM7 plasmid DNA.

- 39 -

The following solutions were used in this procedure: 2x HEBS buffer (280 mM NaCl, 10 mM KCl, 1.5 mM sterile filtered); 0.25 mM CaCl₂ (autoclaved).

Immunoprecipitation

- 5 After 48 to 60 hours medium was exchanged and cells were incubated for additional 12 hours in Cys/Met-free medium containing 200 μ Ci of ³⁵S-translabel. Supernatants were harvested and spun for 15 min at 3000 rpm to remove debris. After addition of protease
- 10 inhibitors leupeptin, aprotinin and PMSF to 2.5 μ g/ml, 50 μ g/ml, 100 μ g/ml respectively, 1 ml of supernatant was incubated with either 10 μ l of packed protein A sepharose alone (rTHY-1envegrire) or with protein A sepharose and 3 μ g of a purified CD4/immunoglobulin fusion protein
- 15 (kindly provided by Behring) (all gp120 constructs) at 4°C for 12 hours on a rotator. Subsequently the protein A beads were washed 5 times for 5 to 15 min each time. After the final wash 10 μ l of loading buffer containing was added, samples were boiled for 3 min and applied on
- 20 7% (all gp120 constructs) or 10% (rTHY-1envegrire) SDS polyacrylamide gels (TRIS pH 8.8 buffer in the resolving, TRIS pH 6.8 buffer in the stacking gel, TRIS-glycin running buffer, Maniatis et al. 1989). Gels were fixed in 10% acetic acid and 10% methanol, incubated with
- 25 Amplify for 20 min, dried and exposed for 12 hours.

The following buffers and solutions were used in this procedure: Wash buffer (100 mM Tris, pH 7.5, 150 mM NaCl, 5 mM CaCl₂, 1% NP-40); 5x Running Buffer (125 mM Tris, 1.25 M Glycin, 0.5% SDS); Loading buffer (10% glycerol, 4% SDS, 4% β -mercaptoethanol, 0.02% bromphenol blue).

Immunofluorescence

293T cells were transfected by calcium phosphate coprecipitation and analyzed for surface THY-1 expression after 3 days. After detachment with 1 mM EDTA/PBS, cells

- 40 -

- were stained with the monoclonal antibody OX-7 in a dilution of 1:250 at 4°C for 20 min, washed with PBS and subsequently incubated with a 1:500 dilution of a FITC-conjugated goat anti-mouse immunoglobulin antiserum.
- 5 Cells were washed again, resuspended in 0.5 ml of a fixing solution, and analyzed on a EPICS XL cytofluorometer (Coulter).

The following solutions were used in this procedure:

- 10 PBS (137 mM NaCl, 2.7 mM KCl, 4.3 mM Na₂HPO₄, 1.4 mM KH₂PO₄, pH adjusted to 7.4); Fixing solution (2% formaldehyde in PBS).

ELISA

- The concentration of gp120 in culture supernatants 15 was determined using CD4-coated ELISA plates and goat anti-gp120 antisera in the soluble phase. Supernatants of 293T cells transfected by calcium phosphate were harvested after 4 days, spun at 3000 rpm for 10 min to remove debris and incubated for 12 hours at 4°C on the 20 plates. After 6 washes with PBS 100 µl of goat anti-gp120 antisera diluted 1:200 were added for 2 hours. The plates were washed again and incubated for 2 hours with a peroxidase-conjugated rabbit anti-goat IgG antiserum 1:1000. Subsequently the plates were washed and 25 incubated for 30 min with 100 µl of substrate solution containing 2 mg/ml o-phenylenediamine in sodium citrate buffer. The reaction was finally stopped with 100 µl of 4 M sulfuric acid. Plates were read at 490 nm with a Coulter microplate reader. Purified recombinant 30 gp120IIIB was used as a control. The following buffers and solutions were used in this procedure: Wash buffer (0.1% NP40 in PBS); Substrate solution (2 mg/ml o-phenylenediamine in sodium citrate buffer).

- 41 -

Use

The synthetic genes of the invention are useful for expressing the a protein normally expressed in mammalian cells in cell culture (e.g. for commercial 5 production of human proteins such as hGH, TPA, Factor VII, and Factor IX). The synthetic genes of the invention are also useful for gene therapy.

- 42 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: SEED, BRIAN

(ii) TITLE OF INVENTION: OVEREXPRESSION OF MAMMALIAN AND VIRAL PROTEINS

(iii) NUMBER OF SEQUENCES: 37

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30B

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/308,286
- (B) FILING DATE: 19-SEP-1994

(viii) ATTORNEY/AGENT INFORMATION:

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- (B) REGISTRATION NUMBER: 30,162
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCGGGCTAG CCACCGAGAA GCTG

24

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 43 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCGAGAAGC TGTGGTGAC CGTGTACTAC GGCGTGCCTG	TGTGGAAGAG AGGCCACCCAC	60
CACCCCTGTTC TGCGCCAGCG ACGCCAAGGC GTACGACACC GAGGTGCACA ACCTGTGGGC		120
CACCCAGGCG TGCGTGCCCCA CCGACCCCAA CCCCCAGGAG GTGGAGCTCG TGAACGTGAC		180
CGAGAACTTC AACATG		196

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCACCATGTT GTTCTTCCAC ATGTTGAAGT TCTC	34
---------------------------------------	----

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GACCGAGAAC TTCAACATGT CGAACAAACAA CAT	33
---------------------------------------	----

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGGAAGAAC ACATGGTGGG GCAGATGCAT GAGGACATCA TCAGCCTGTG GGACCAAGAGC	60
CTGAAGCCCT GCGTGAAGCT GACCCCTGT GCGTGACCTG AACTGCACCG ACCTGAGGAA	120
CACCAACCAAC ACCAACACAG CACCGCCAAC AACAAACAGCA ACAGCGAGGG CACCATCAAG	180

- 44 -

GGCGGGCGAGA TG 192

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTGAAGCTG CAGTTCTTCA TCTCGCCGCC CTT 33

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGAACTGC AGCTTCACAA TCACCCACCAG C 31

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AACATCACCA CCAGCATCCG CGACAAGATG CAGAAGGAGT ACGCCCTGCT GTACAAGCTG 60

GATATCGTGA GCATCGACAA CGACACCCACC AGCTACCGCC TGATCTCCTG CAACACCCAGC 120

GTGATCACCC AGGCCTGCCA CAAGATCAGC TTCTGAGCCA TCCCCATCCA CTACTGCGCC 180

CCCCCCGGCT TCGCC 195

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 45 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAACTTCTTG TCGGGGGCGA AGCCGGCGGG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGCCCCCGC CGGCTTCGCC ATCCTGAAGT GCAACGACAA GAAGTTC

47

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCGACAAAGA AGTTCAGCGG CAAGGGCAGC TCCAAGAACG TGAGCACCCT GCAGTGCACC

60

CACGGCATCC GGCGGGTGGT GAGCACCCAG CTCTGCTGA ACGGCAGCCT GGCGGAGGAG

120

GAGGTGGTGA TCCGCAGCGA GAACTTCACC GACAACGCCA AGACCATCAT CGTGCACCTG

180

AATGAGAGCG TGCAGATC

198

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGTTGGGACG CGTGCAGTTG ATCTGCACGC TCTC

34

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 46 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGAGCGTGC AGATCAACTG CACCGGTCCC

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACTGCACGC GTCCCAAATA CAACAAGCGC AAGCGCATCC ACATCGGCC CGGGCGCGCC

60

TTCTACACCA CCAAGAACAT CATCGGCACC ATCCTCCAGG CCCACTGCAA CATCTCTAGA

120

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGTTCCAC TTGGCTCTAG AGATGTTGCA

30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCAACATCTC TAGAGCCAAG TGGAACGAC

29

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 47 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCCAAAGTGGAA	ACGACACCCCT	GCGCCAGATC	GTGAGCAAGC	TGAAGGAGCA	GTTCAAGAAC	60
AAGACCACATCG	TGTTCACCCAG	ACGAGCGGGG	CCGACCCCGA	GATCGTGATG	CACAGCTTCA	120
ACTGGGGCGG C						

(2) INFORMATION FOR SEQ ID NO:18: 131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCAGTAGAAAG AATTGCCGC CGCAGTTGA

(2) INFORMATION FOR SEQ ID NO:19: 29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCAACTGGGG CGGGAAATTTC TTCTACTGC

(2) INFORMATION FOR SEQ ID NO:20: 29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCGAATTCT	TCTACTGC	AA CACCAGCCCC	CTGTTCAACA	GCACCTGGAA	CGGCAACAAAC	60
ACCTGGAAACA	ACACCACCGG	CAGCAACAAAC	AATATTACCC	TCCAGTGC	AA GATCAAGCAG	120
ATCATCAACA	TGTGGCAGGA	GGTGGGCAAG	GCCATGTACG	CCCCCCCCAT	CGAGGGCCAG	180
ATCCGGTGCA	GCAGC					

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- 48 -

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGACCGGT GATGTTGCTG CTGCACCGGA TCTGGCCCTC

40

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGAGGGCCAG ATCCGGTGCA GCAGCAACAT CACCGGTCTG

40

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AACATCACCG GTCTGCTGCT GCTGCTGACC CGGACGGCGG CAAGGACACC GACACCAACG

60

ACACCGAAAT CTTCCGGGAC GGCGGCAAGG ACACCAACGA CACCGAAATC TTCCGCCCCG

120

GCGGCGGCCA CATGCGCGAC AACTGGAGAT CTGAGCTGTA CAAGTACAAG GTGGTGACGA

180

TCGAGCCCCCT GGGCGTGGCC CCCACCAAGG CCAAGCGCGC GGTGGTGCAG CGCGAGAACG

240

GC

242

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 49 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGGGGGCGGC CGCTTTAGCG CTTCTCGCGC TGCACCAC

(2) INFORMATION FOR SEQ ID NO:25:

38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGGGGGGAT CCAAGCTTAC CATGATTCCA GTAATAAGT

(2) INFORMATION FOR SEQ ID NO:26:

39

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAATCCAG TAATAAGTAT AACATTATTA TTAAGTGTAT TACAAATGAG TAGAGGACAA
AGAGTAATAA GTTAAACAGC ATCTTTAGTA AATCAAAATT TGAGATTAGA TTGTAGACAT
GAAAATAATA CAAATTTGCC AATACAACAT GAATTTTCAT TAACG

60

120

165

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGCGGGGAAT TCACCGCGTTA ATGAAAATTC ATGTTG

36

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 50 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGCGGATCCA CGCGTGAAAAA AAAAAAAACAT

30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGTGAAAAAA AAAAAACATGT ATTAAGTGGGA ACATTAGGAG TACCAGAACCA TACATATAGA

60

AGTAGAGTAA TTTGTTTAGT GATAGATTCA TAAAAGTATT AACATTAGCA AATTTTACAA

120

CAAAAGATGA AGGAGATTAT ATGTGTGAG

149

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCCGAATTAG AGCTCACACA TATAATCTCC

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGCGGATCCC AGCTCAGAGT AAGTGGACAA

30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 51 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCAGACTAA GTGGACAAAA TCCAACAAGT AGTAATAAAA CAATAATGT AATAAGAGAT	60
AAATTAGTAA AATGTGAGGA ATAAGTTTAT TAGTACAAAA TACAAGTTGG TTATTATTAT	120
TATTATTAAG TTTAAGTTT TTACAAGCAA CAGATTTAT AAGTTATGA	170

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGCGAATTCTG CGGCCGCTTC ATAAACTTAT AAAATC	36
--	----

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCGAGATCC ATTGTGCTCT AAAGGAGATA CCCGCCAGA CACCCCTCACCC TGCGGTGCC	60
AGCTGCCAG GCTGAGGCAGA GAGAAGGCCA GAAACCATGC CCATGGGTC TCTGCAACCG	120
CTGGCCACCT TGTACCTGCT GGGGATGCTG GTCGCTTCGG TGCTAGCCAC CGAGAAAGCTG	180
TGGGTGACCG TGTACTACGG CGTGCCCCGTG TGGAAAGGAGG CCACCAACAC CCTGTTCTGC	240
GCCAGCGACG CCAAGGCAGA CGACACCGAG GTGCACAAACG TGTGGGCCAC CCAGGGTGC	300
GTGCCCAACCG ACCCCAACCC CCAGGAGGTG GAGCTCGTGA ACGTGACCGA GAACTTCAAC	360
ATGTGGAAGA ACAACATGGT GGAGCAGATG CATGAGGACA TCATCAGCCT GTGGGACCA	420
AGCCTGAAGC CCTGCGTGA GCTGACCCCC CTGTGCGTGA CCCTGAACCTG CACCGACCTG	480
AGGAACACCA CCAACACCAA CAACAGCACC GCCAACACA ACAGAACACG CGAGGGCACC	540
ATCAAGGGCG GCGAGATGAA CAACTGCAGC TTCAACATCA CCACCAAGCAT CCCGGACAAG	600
ATGCAGAAGG AGTACGCCCT GCTGTACAAG CTGGATATCG TGAGCATCGA CAACCGACAGC	660
ACCAGCTACC GCCTGATCTC CTGCAACACC AGCGTGATCA CCCAGGCCTG GCCCAAGATC	720
AGCTTCGAGC CCATCCCCAT CCACTACTGC GCCCCCGCCG CCTTCGCCAT CCTGAAGTGC	780
AACGACAAGA AGTTCAAGCGG CAAGGGCAGC TGCAAGAACG TGAGCCACCGT CGAGTGCACC	840

- 52 -

CACGGCATCC	GGCCGGTGGT	GAGCACCCAG	CTCCTGCTGA	ACGGCAGCCT	GGCCGAGGAG	900
GAGGTGGTGA	TCCGCAGCGA	GAACATTCACC	GACAACGCCA	AGACCATCAT	CGTGCACCTG	960
AATGAGAGCG	TGCAGATCAA	CTGCACCGGT	CCCAACTACA	ACAAGCGCAA	GCGCATCCAC	1020
ATCGGCCCCG	GGCGCGCCTT	CTACACCACC	AAGAACATCA	TCGGCACCAT	CCGCCAGGCC	1080
CACTGCAACA	TCTCTAGAGC	CAAGTGGAAC	GACACCTGTC	GCCAGATCGT	GAGCAAGCTG	1140
AAGGAGCAGT	TCAAGAACAA	GACCATCGTG	TTCAACCAGA	GCAGCGGCGG	CGACCCCCAG	1200
ATCGTGATGC	ACAGCTTCAA	CTGCAGCGGC	GAATTCTTCT	ACTGCAACAC	CAGCCCCCTG	1260
TTCAACAGCA	CCTGGAACGG	CAACAACACC	TGGAACAACA	CCACCCGGAG	CAACAACAAAT	1320
ATTACCCCTCC	AGTGCAAGAT	CAAGCAGATC	ATCAACATGT	GGCAGGAGGT	GGGCAAGGCC	1380
ATGTACGCCC	CCCCCATCGA	GGGCCAGATC	CGGTGCAGCA	GCAACATCAC	CGGTCTGCTG	1440
CTGACCCGCG	ACGGCGGCAA	GGACACCGAC	ACCAACGACA	CCGAAATCTT	CCGCCCCGGC	1500
GGCGCGACCA	TGCGCGACAA	CTGGAGATCT	GAGCTGTACA	AGTACAAGGT	GGTGACGATC	1560
GAGCCCCCTGG	GGTGGCCCC	CACCAAGGCC	AAGGCCCGCG	TGGTGCAGCG	CGAGAACGCC	1620
TAAAGCGGCC	GC					1632

(2) INFORMATION FOR SEQ ID NO:35:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACCGAGAAGC	TGTGGGTGAC	CGTGTACTAC	GGCGTGGCCCG	TGTGGAAGGA	GGCCACCAACC	60
ACCCCTGTTCT	GCGCCAGCGA	CGCCAAGGCG	TACGACACCG	AGGTGCACAA	CGTGTGGGCC	120
ACCCAGGCCT	GGGTGCCAC	CGACCCCAAC	CCCCAGGAGG	TGGAGCTCGT	GAACGTGACC	180
GAGAACTTCA	ACATGTGGAA	GAACAACATG	CTGGAGCAGA	TGCATGAGGA	CATCATCAGC	240
CTGTGGGACC	AGAGCCTGAA	GCCCTGCGTG	AAGCTGACCC	CCCTGTGCGT	GACCCCTGAAC	300
TGCACCGACC	TGAGGAACAC	CACCAACACC	AAACAACAGCA	CCGCCAACAA	CAACAGCAAC	360
AGCGAGGGCA	CCATCAAGGG	CGGGGAGATG	AAGAACTGCA	CCTTCACAT	CACCAACCAGC	420
ATCCCGGACA	AGATGCAGAA	GGAGTACGCC	CTGCTGTACA	AGCTGGATAT	CGTGAGCATE	480
CACAACGACA	GCACCCAGCTA	CCGCCTGATC	TCCTGCAACA	CCAGCGTGAT	CACCCAGGCC	540
TGCCCCAAGA	TCAGCTTCGA	GCCCATCCCC	ATCCACTACT	GCGCCCCCGC	CGGCTTCGCC	600
ATCCTGAAGT	GCAACGACAA	GAAGTTCAAC	GGCAAGGGCA	GCTGCAAGAA	CGTGACCAACC	660

- 53 -

GTGCAGTGCA CCCACGGCAT CCGGCGGTG GTGAGGCACCC AGCTCTGCT GAAACGGCAGC	720
CTGGCCGAGG AGGAGGTGGT GATCCGCAGC GAGAACCTCA CCGACAACGC CAAGACCATC	780
ATCGTGCACC TGAATGAGAG CGTGCAGATC AACTGCACGC GTCCCAACTA CAACAAGCGC	840
AAGCGCATCC ACATCGGCC CGGGCGGCC TTCTACACCA CCAAGAACAT CATCGGCACC	900
ATCCGCCAGG CCCACTGCAA CATCTCTAGA GCCAAGTGGA ACGACACCCCT GCGCCAGATC	960
GTGAGCAAGC TGAAGGGAGCA GTTCAAGAAC AAGACCATCG TGTTCAACCA GAGCAGCGGC	1020
GGCGACCCCCG AGATCGTGAT GCACAGCTTC AACTGGGGG GCGAATTCTT CTACTGCAAC	1080
ACCAGCCCCC TGTTCAACAG CACCTGGAAC GGCAACAAACA CCTGGAACAA CACCACCGC	1140
ACCAACAAACA ATATTACCCCT CCAGTGCAAG ATCAAGCAGA TCATCAACAT GTGGCAGGAG	1200
GTGGCAAGG CCATGTACGC CCCCCCCCATC GAGGGCCAGA TCCGGTGCAG CAGCAACATC	1260
ACCGGTCTGC TGCTGACCCG CGACGGCGGC AAGGACACCG ACACCAACGA CACCGAAATC	1320
TTCCGGCCCG GCGGCGGCCA CATGCGCGAC AACTGGAGAT CTGAGCTGTA CAACTACAAG	1380
GTGGTACGA TCGAGCCCCT GGGCGTGGCC CCCACCAAGG CCAAGCGCCG CGTGGTGCAG	1440
CGCGAGAACG GGGCCGCCAT CGGCCCCCTG TTCCCTGGGCT TCCTGGGGGC GGCGGGCAGC	1500
ACCATGGGGG CGGCCAGCGT GACCCCTGACC GTGCAGGCC GCCTGCTCCT GAGCGGCATC	1560
GTGCAGCAGC AGAACAAACCT CCTCCCGGCC ATCGAGGCC AGCAGCATAT GCTCCAGCTC	1620
ACCGTGTGGG GCATCAAGCA GCTCCAGGCC CGCGTGCTGG CGCTGGAGCG CTACCTGAAG	1680
GACCAGCAGC TCCTGGGCTT CTGGGGCTGC TCCGGCAAGC TGATCTGCAC CACCACGGTA	1740
CCCTGGAACG CCTCCTGGAG CAACAAGAGC CTGGACGCCA TCTGGAACAA CATGACCTGG	1800
ATGCAGTGGG AGCGCGAGAT CGATAACTAC ACCAGCCTGA TCTACAGCCT GCTGGAGAAG	1860
AGCCAGACCC AGCAGGAGAA GAACGAGCAG GAGCTGCTGG AGCTGGACAA CTGGGGCGAGC	1920
CTGTGAACT GGTTCGACAT CACCAACTGG CTGTGGTACA TCAAAATCTT CATCATGATT	1980
GTGGGGGGCC TGGTGGGCCT CGGCATCGTG TTGGCCGTGC TGAGCATCGT GAAACGGCGTG	2040
CGCCACGGCT ACAGCCCCCT GAGCCTCCAG ACCCGGGCCC CGCTGGGGG CGGGCCCCGAC	2100
CGCCCCCGAGG GCATCGAGGA GGAGGGGGC GAGCGCGACC GCGACACCAAG CGGCAGGCTC	2160
GTGCACGGCT TCCTGGCGAT CATCTGGTC GACCTCCGCA GCCTGTTCTT GTTCAGCTAC	2220
CACCAACCGCG ACCTGCTGCT GATGGCGCC CGCATCGTGG AACTCCTAGG CCGCCGGGC	2280
TGGGAGGTGC TGAAGTACTG GTGGAACCTC CTCCAGTATT GGAGCCAGGA GCTGAAGTCC	2340
AGCGCCGTGA GCCTGCTGAA CGCCACCGCC ATGCCCGTGG CGGAGGGCAC CGACCCCGTG	2400
ATCGAGGTGC TCCAGAGGGC CGGGAGGGCG ATCCTGCACA TCCCCACCCG CATCCGCCAG	2460
GGGCTCGAGA GGGCGCTGCT G	2481

- 54 -

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGAATCCAG	TAATAAGTAT	AACATTATTA	TTAAGTGTAT	TACAAATGAG	TAGAGGACAA	60
AGAGTAATAA	GTTAACAGC	ATGTTAGTA	AATCAAAATT	TGAGATTAGA	TTGTAGACAT	120
GAAAATAATA	CACCTTGCC	AATACAACAT	GAATTTCAT	TAACCGGTGA	AAAAAAAAAA	180
CATGTATTAA	GTGGAACATT	AGGAGTACCA	GAACATACAT	ATAGAAGTAG	AGTAAATTG	240
TTTAGTGATA	GATTCAAAA	AGTATTAACA	TTAGCAAATT	TTACAACAAA	AGATGAAGGA	300
GATTATATGT	GTGAGCTCAG	AGTAAGTGG	CAAATCCAA	CAAGTAGTAA	AAAAACAATA	360
AATGTAATAA	GAGATAAATT	AGTAAAATGT	GGAGGAATAA	GTITATTAGT	ACAAAATACA	420
AGTTGGTTAT	TATTATTATT	ATTAAGTTA	AGTTTTTAC	AAGAACAGA	TTTTATAAGT	480
TTATGA						486

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGAACCCAG	TCATCAGCAT	CACTCTCCTG	CTTTCAGTCT	TGCAGATGTC	CCGAGGACAG	60
ACGGTGATCA	GCCTGACAGC	CTGCCCTGGTG	AACAGAACCT	TCGACTGGAC	TGCCGTATG	120
ACAATAACAC	CAACTTGCCC	ATCCAGCATG	AGTTCAGCCT	GACCCGAGAG	AAGAAGAAC	180
ACGTGCTGTC	AGGCACCCCTG	GGGGTTCCCG	AGCACACTTA	CCGCTCCCGC	GTCAACCTTT	240
TCAGTGACCG	CTTTATCAAG	GTCTTACTC	TAGCCAACCT	GACCACCAAG	GATGAGGGCG	300
ACTACATGTG	TGAACCTCGA	GTCTCGGGCC	AGAATCCAC	AAGCTCCAAT	AAAACATATCA	360
ATGTGATCAG	AGACAAAGCTG	GTCAAGTGTG	GTGGCATAAG	CCTGCTGGTT	AAAAACACTT	420
CCTGGCTGCT	GCTGCTCCTG	CTTCCCTCT	CCTTCCTCCA	AGCCACGGAC	TTCATTTCTC	480
TGTCA						485

What is claimed is:

- 55 -

1. A synthetic gene encoding a protein normally expressed in mammalian cells wherein at least one non-preferred or less preferred codon in the natural gene encoding said mammalian protein has been replaced by a preferred codon encoding the same amino acid.
5
2. The synthetic gene of claim 1 wherein said synthetic gene is capable of expressing said mammalian protein at a level which is at least 110% of that expressed by said natural gene in an in vitro mammalian cell culture system under identical conditions.
10
3. The synthetic gene of claim 1 wherein said synthetic gene is capable of expressing said mammalian protein at a level which is at least 150% of that expressed by said natural gene in an in vitro cell culture system under identical conditions.
15
4. The synthetic gene of claim 1 wherein said synthetic gene is capable of expressing said mammalian protein at a level which is at least 200% of that expressed by said natural gene in an in vitro cell culture system under identical conditions.
20
5. The synthetic gene of claim 1 wherein said synthetic gene is capable of expressing said mammalian protein at a level which is at least 500% of that expressed by said natural gene in an in vitro cell culture system under identical conditions.
25
6. The synthetic gene of claim 1 wherein said synthetic gene is capable of expressing said mammalian protein at a level which is at least ten times that expressed by said natural gene in an in vitro cell culture system under identical conditions.
30

- 56 -

7. The synthetic gene of claim 1 wherein at least 10% of the codons in said natural gene are non-preferred codons.

8. The synthetic gene of claim 1 wherein at least 5 50% of the codons in said natural gene are non-preferred codons.

9. The synthetic gene of claim 1 wherein at least 50% of the non-preferred codons and less preferred codons present in said natural gene have been replaced by 10 preferred codons.

10. The synthetic gene of claim 1 wherein at least 90% of the non-preferred codons and less preferred codons present in said natural gene have been replaced by preferred codons.

15 11. The synthetic gene of claim 1 wherein said protein is a retroviral or lentiviral protein.

12. The synthetic gene of claim 11 wherein said protein is an HIV protein.

13. The synthetic gene of claim 12 wherein said 20 protein is selected from the group consisting of gag, pol, and env.

14. The synthetic gene of claim 13 wherein said protein is gp120 or gp160.

15. The synthetic gene of claim 1 wherein said 25 protein is a human protein.

- 57 -

16. A method for preparing a synthetic gene
encoding a protein normally expressed by mammalian cells,
comprising identifying non-preferred and less-preferred
codons in the natural gene encoding said protein and
5 replacing one or more of said non-preferred and less-
preferred codons with a preferred codon encoding the same
amino acid as the replaced codon.

Syngp120mn

1 CTCGAGATCC ATTGTGCTCT AAAGGGAGATA CCGGGGCCAGA CACCCCTCACC
 51 TCGGGTGCCTC AGCTGCCAG GCTGAGCCAA GAGAAGGGCA GAAACCATGC
 101 CCATGGGGTC TGTGCAACCG CTGGCCACCT TGTACCTGCT CGGGATGCTG
 151 CTGGCTTCCG TGTAGCCAC CGAGAAGCTG TGGGTGACCG TGTACTACGG
 201 CGTGCCCCGTG TGAAGGGAGG CCACCCACAC CCTGTTCTGC CGCAGGGACG
 251 CCAAGGGATA CACACCCAG GTGACAAACG TGTGGCCAC CGAGGGGTGC
 301 GTGCCCCACCG ACCCCAACCC CGAGGAGGTG GAGCTCTGA ACGTGACCGA
 351 GAACTTCAAC ATGTTGAAGA ACAACATGGT GGAGGAGATG CATGAGGACA
 401 TCATGAGCT GTGGGACCAAG AGCCTGAAGC CCTGGGTGAA GCTGACCCCC
 451 CTGTGCTGA CCTGAAACTS CACCCACCTG AGGAACACCA CCAACACCAA
 501 CAACAGCACC GCAACACAA ACACCAACAG CGAGGGCACCC ATCAAGGGCG
 551 CGGAGATGAA CAACTGGAGC TTCAACATCA CGACCGAGAT CGGGGACAAG
 601 ATGGAGAAGG ATGAGGCGCT GTGTACAAG CTGGATATCG TTAGCATCGA
 651 CAACGACAGC ACCAGCTACC CCTGTATCTC CTGCAACACCC AGCGTGTATCA
 701 CCCAGGCCTG QCCCAAGATC AGCTTGAGC CCATCCCCAT CGACTACTGC
 751 GCCCCCCCGG CCTTCCCAT CCTGAAGTSC AACGACAAGA AGTTTACGGG
 801 CAAGGGCAGC TCGAAGAACG TGAGCACCGT CGAGTGCACC CACGGCATCC
 851 CGCCGGTGGT QAGCACCCAG CCTCTGCTGA ACGGCAGCCT GGGGGAGGAG
 901 GAGGTGCTGA TCCGCAGCGA GAACTTCACC GACAACGCCA AGACCATCAT
 951 CCTGCACCTG AATGAGAGCG TCGAGATCAA CTGCAACGGT CCCAACTACA
 1001 ACAAGGCAAA QGGCATCCAC ATGGGCCCCG GGGCGCCCTT CTACACCACC
 1051 AAGAACATCA TCGGCACCAT CGCCAGGCG CACTGCAACA TCTCTAGAGC
 1101 CAAGTGGAAC GACACCTG CCTGAAACCG GAGGCGGGGG CGACCCCCAG
 1151 TCAAGAACAA GACCATGCG TTCAACCGAGA CGAGGGGGGG CGACCCCCAG
 1201 ATCGTGTATGC ACAGCTTCAA CTGGGGGGGC GAATTCTTCT ACTGCAACAC
 1251 CAGCCCCCTG TTCAACAGCA CCTGGAAACCG CAACAAACCC TGGAAACAAACA
 1301 CCACCCCGAG CAACAAACAT ATTACCCCTC AGTGCAGAT CAAGCAGATC
 1351 ATCAACATCT CGCAGGAGT CGGCAAGGCC ATGTACCCCC CCCCCATCGA
 1401 GGGCCAGATC CGGTGAGCA GCAACATCAC CGGTCTGCTG CTGACCCCCG
 1451 ACGGGGGCAA CGACACCGAC ACCAACGACA CGGAAATCTT CCCCCCGGGC

FIG 1
(SHEET 1 OF 4)

2/12

1501 CGCGGCGACA TGGCGACAA CTGGAGATCT GAGCTGTACA AGTACAAAGGT
1551 GGTGACCGATC GAGCCCTGG CCTTGCCCC CACCAAGGCC AAGCCCGCC
1601 TGGTGCAGCG CAGAAGGCC TAAAGGGCC SC (SEQ ID NO:34)

FIG 1
(SHEET 2 OF 4)

3/12

Syngp160mn

1 AUCGAGAAAGC TGTGGGTGAC CTTTCTACTAC CGCGTTCAGG TGTGGAAAGGA
 51 GGCACCCACCC AGCTTCTTCT AGGCCAGCGA GCGCAAGGGG TACGACACCC
 101 ATGGTGACCAA CTGTGCGGCC ACCGAGGCTT GGTGCGCAC CGACCCCCAAC
 151 CGCCGAGGAGG TGGAGCTCTT GAACGTCAGG CAGAACTTCA ACATGTGGAA
 201 GAGAAACATG CTGGAGCAGA TGTATGAGG CTCATCAGG CTGTGGGACC
 251 AGAGCTGAA GCGCTTCCTG AAGCTGACCS CCTGTGCGCT GACCTCAAC
 301 TGCACCCAGC TGGAAACACG CACCAACACG AACAAACAGCA CGGCCGAGCA
 351 CAACACAAAC AGCGAGGGCA CCTCAAGGG CGCCGAGATG AAGAACTCCA
 401 CCTTCACAT CACCAACAGG ATCCCGACCA AGATCCAGAA CGAUWACCCC
 451 CTCTGTGACA AGCTGATAT CCTGAGGATC CACAAACACA CGACGGAGCTA
 501 CGCGCTGATC TGTGCGACA CGACGGCTAT CGACGGAGGC TCGGGCAAGCA
 551 TGACCTTCA GCGCGAGGGG ATGCACTACT CGCGGGGGCG CGCGTTGGCC
 601 ATCGCTAACT GCAACGACAA GAACTTCAGG CGCAAGGGCA CCTGCAAGAA
 651 CCTGACCCACG CTGAGCGCA CGACGGCGAT CGCGGGCGTG CTGAGGACCC
 701 AGCTCTCTG GAAUUGCGAGG CTGGGGGAGG AGGAGGTGTT CTCCTTCAGC
 751 GAGACTTCA CGGACAAACCG CAAAGACCAT ATCGTGCACG TGAATGAGAG
 801 CGTGAGAGT AACTGACCGC CGGCGAACTA CAACAAAGCC AAGGCGATCC
 851 ACATGGGGCC CGCGGGGGCG TTCTACACCA CGAAGAACAT CTCGGACCC
 901 ATCGGGGAAAG CGGACTGGAA CATCTTCTAGA CGCAACTGGA ACGACACCT
 951 CGCGGAGATG GTGAGGAAAGT TGAAGGAGCA CCTCAAGAAC AAGACCGATCG
 1001 TGTTCACCA GAGGAGGGG CGCGGGGGCG AGATCTGAT CGACAGCTTC
 1051 AACCTGGGGG GCGAATTCTT CTACTGCAAC ACCAGGGGGG TGTGCAACAC
 1101 CGCTGGAAC GCGAACAAACA CCTGAAACAA CACCCGGGGG ACCAACAAACA
 1151 ATATTAACCT CGAATGCAAG ATGAAAGGAA TGTCAACAT CGCGGAGGAG
 1201 CTGGGGCAAGG CGATCTACCG CGCGGGGGCG TACGGGGAGA CGCGGGCGAG
 1251 CGCGAACATG ACCGCTTCTG TGTGACCC CGACGGGGCG AAGTACACCC
 1301 ACACCGGCUA CACCGAAATG CGCGGGGGCG CGCGGGGAGA CTCGCGCGAC
 1351 AAUTGGAGAT CTGAGCTGTA CGAATGACAG ATGGTGACCA TCGAGGGGGT
 1401 CGCGGGGGCG CGGACCAAGG CGAAGGGGGCG CGCGGGCGAG CGCGAGAAGC

FIG. 1
(SHEET 3 OF 4)

1451 GGGGCCCCAT CCCCCCCCCC TTCCCTGGGCT TCCCTGGGGCC GGGGGGGAGC
1501 ACCATGGGGG CCCCCCAGGCT GACCCCTGACC CTGCAGGGCC CCTTGCTCT
1551 GAGCGGGCATC GTGGAGGAGC AGAACAAACCT CCTCCGGGGC ATCGAGGGCC
1601 AGCAGGATAT GTCAGGAGCT ACCCTGTGGG GCACTAAGCA GCTCCAGGCC
1651 CCCTTGCTGG CTCCTGGAGC CTACCTGAAG GACCAAGAGC TCCCTGGGCTT
1701 CTGGGGCTGC TCCCCGAGG TGATCTGGAC CACGACGCTA CCCTGGAAACG
1751 CCTCCCTGGAG CAACAAAGAGC CTGGACGACA TCTGGAAACAA CATGACCTGG
1801 ATGCAGTGGG AGCCCGAGAT CCATAACTAC ACCAGGCTGA TCTACAGGCT
1851 CTGGAGAAG AGCCAGACCC AGCAGGAGAA GAACGACCAAG GAGCTGGCTGG
1901 ACCTGGACAA CTGGGGGAGC CTCTGGAACT CGTTGGACAT CACCAACTGG
1951 CTCTGGTACA TCTAAATCTT CATCATGATT CTGGGGGGCC TGTGGGGCT
2001 CCCCATGGCTT TCCCCCTGC TGTGGATCTT GAAACCCCTG CCCCCAGGCT
2051 ACAGGGGGCT GAGGCTCCAG ACGGGGGGGC CCTTGCGGGC GGGGGGGCAC
2101 CCCCCGAGG GCACTGAGGA GGAGGGCGGC GAGGCGGACC GCGACACCAAG
2151 CGGCAGGCTC GTGGACGCGCT TCTGGCGAT CATCTGGTC GACCTGGCA
2201 CCCTTTCTT GTTCAGGCTAC CACCAACCGC ACCTGCTGCT GATCCCCCGC
2251 CGCATCGTGG AACTCTAGG CCGCCGGGGC TGGGAGGTGC TGAAGTACTG
2301 CTGGAACCTC CTCCAGTATT GGAGCCAGGA CCTGAACTCC AGCGGGGTGA
2351 CCCTGCTGAA CCCCCACCCCG ATCGCCCGTG GGGAGGGCAC GCAACCCCTG
2401 ATGGAGGTGC TCCAGAGGGC GGGGAGGGCG ATCCCTGACA TCCCCACCCG
2451 CATCCGCCAG AGGCTCGAGA GGGGGCTGCTGCTG (SEQ ID NO:3)

5/12

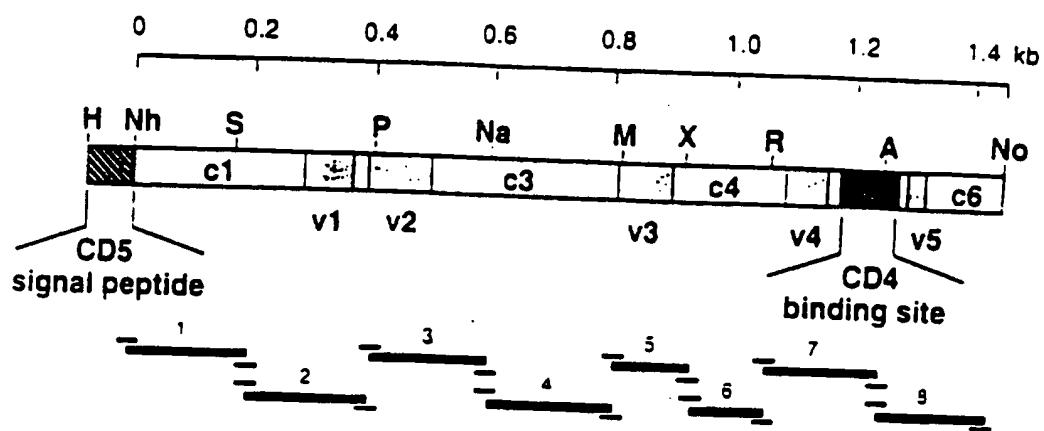


FIGURE 2

6/12

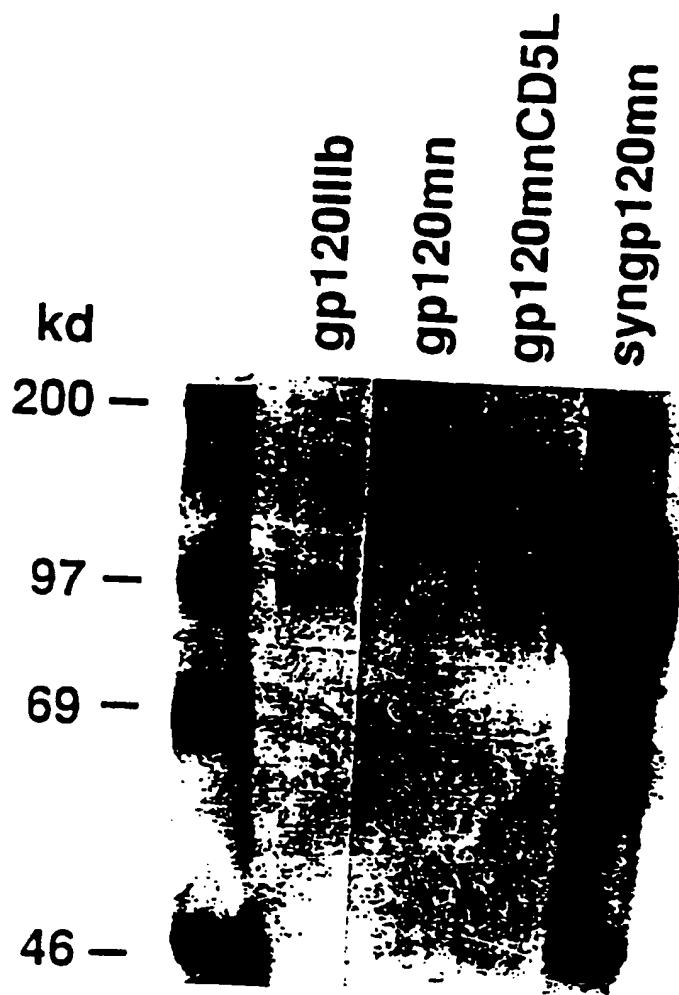


FIGURE 3

7/12

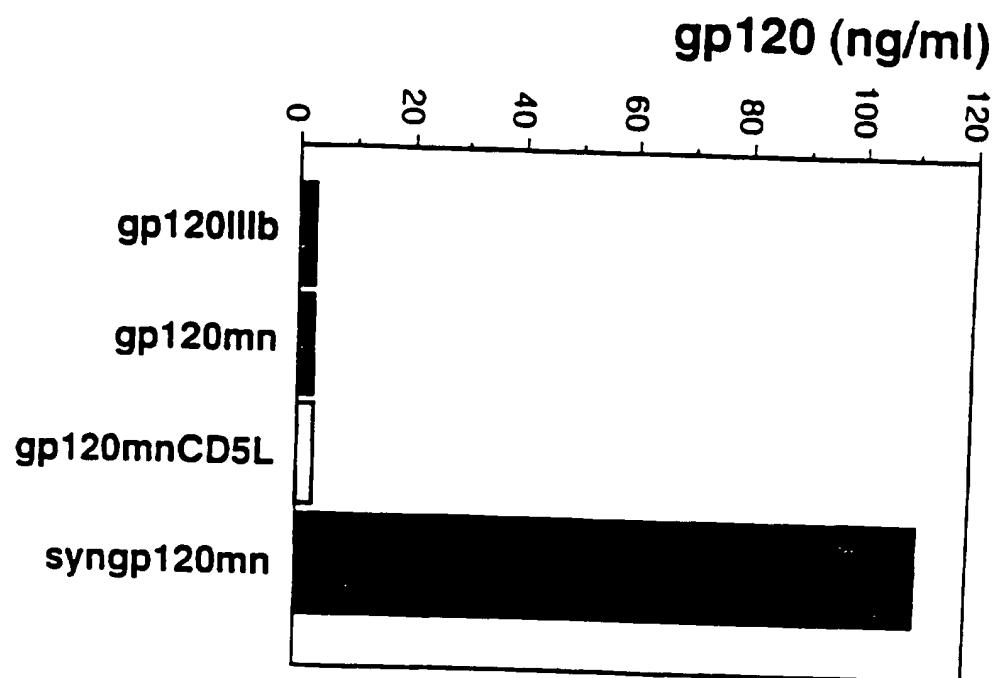


FIGURE 4

8/12

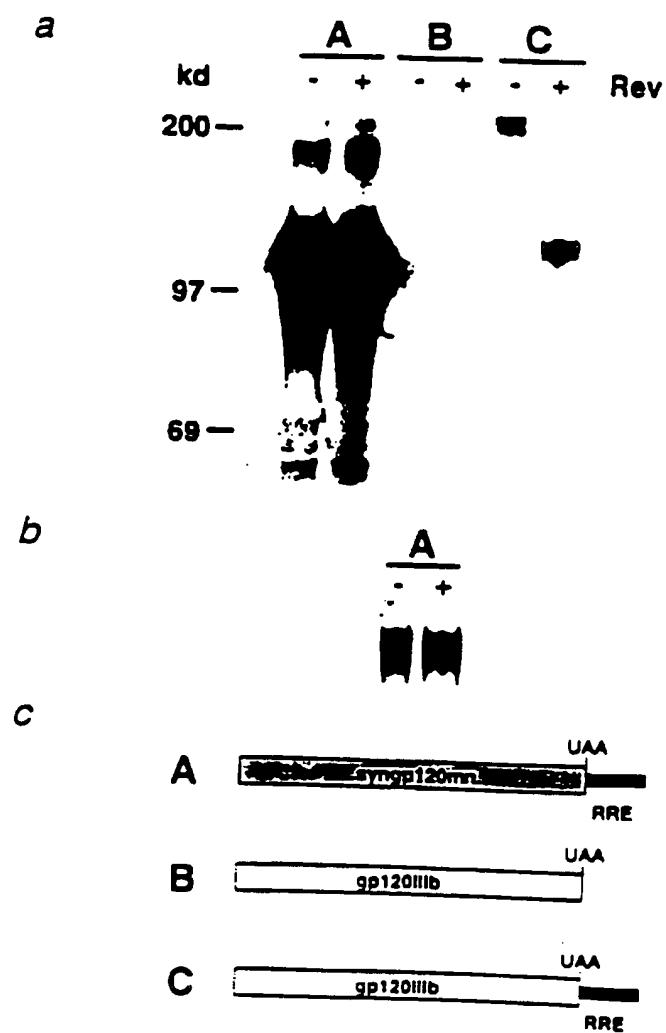


FIGURE 5

9/12

<i>Se₅</i> ID# 36 env	M	N	P	V	I	S	I	T	L	L	S	R	G	Q
<i>Se₅</i> ID# 37-wt	>atg	aat	cca	gtt	ata	agt	ata	aca	tta	tta	atg	gtt	caa	atg
env	R	V	I	S	L	T	A	C	L	V	N	L	R	D
wt	aga	gtt	ata	agt	tta	aca	gtt	tta	gtt	aaa	tta	atg	tgt	aaa
env	E	N	N	T	N	L	P	I	Q	H	E	F	S	L
wt	gaa	aat	aat	aca	cct	ttg	cca	ata	caa	cat	gaa	ttt	tca	ttt
env	H	V	L	S	G	T	L	G	V	P	E	H	T	Y
wt	cat	gtt	tta	agt	ggg	aca	tta	ggg	gtt	ccc	gag	ttt	ttt	ttt
env	F	S	D	R	F	I	K	V	L	T	L	A	N	F
wt	ttt	agt	gtt	aga	tcc	ata	aaa	gtt	tta	aca	tca	ttt	aca	ttt
env	D	Y	M	C	E	L	R	V	S	G	Q	N	P	T
wt	ttc	atg	tat	atg	tgt	ttt	atc	aag	gtc	ttt	act	ttt	acc	ttt
env	N	V	I	R	D	K	L	V	K	C	C	I	S	N
wt	aat	gtt	ata	aga	gat	aaa	tta	gtt	aaa	tgt	ggg	ata	atg	tta
env	S	W	L	I.	I.	I.	I.	S	L	S	F	I.	Q	A
wt	agt	tgg	tta	tta	tta	tta	tta	gtt	gtt	tgt	gtt	tta	gtt	tta
env	I.	.	•	•	•	•	•	•	•	•	•	•	•	•
wt	tta	tga	ctg	tga	ctg	ctg	ctg	ctg	ctg	ctc	ctc	ctc	ctc	ctc

FIGURE 6

10/12

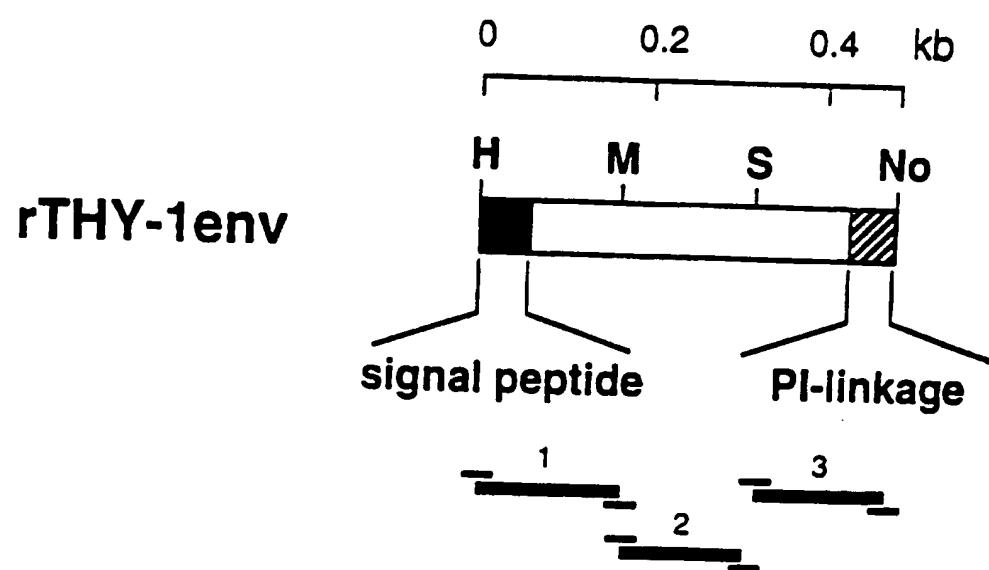


FIGURE 7

11/12

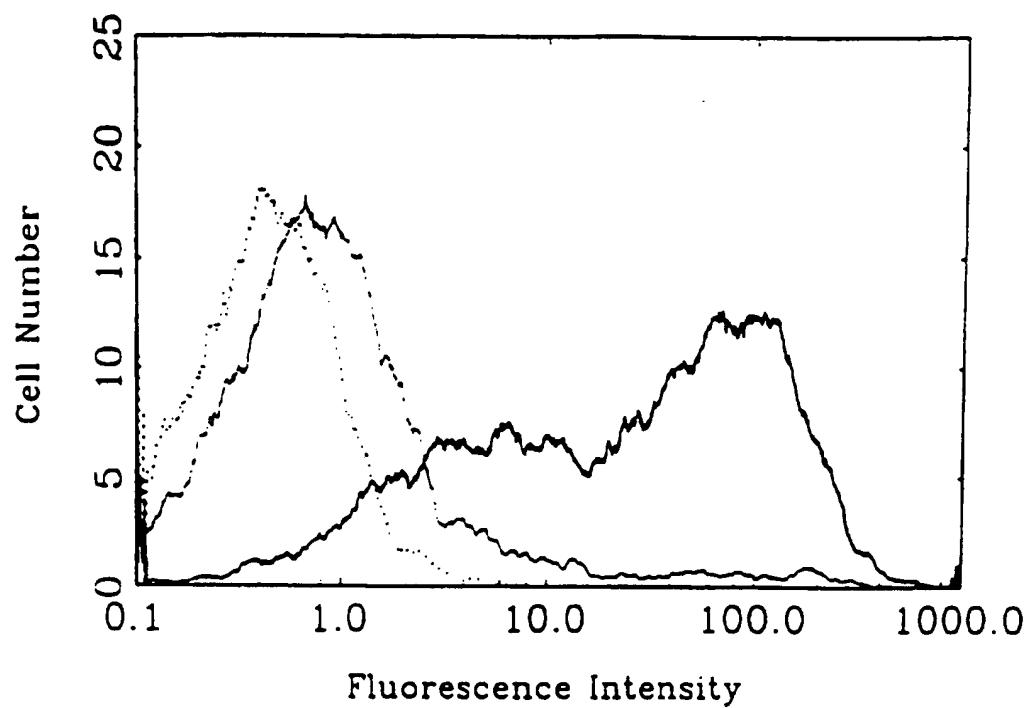


FIGURE 8

12/12

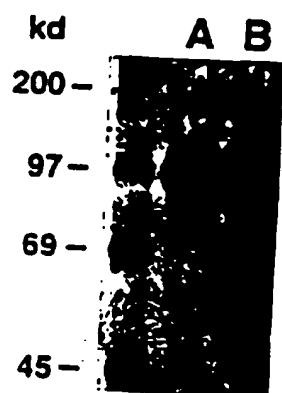
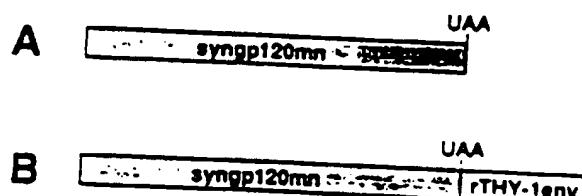
a*b*

FIGURE 9

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/11511

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : Please See Extra Sheet.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Please See Extra Sheet.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US, A, 5,270,171 (CERCEK ET AL.) 14 December 1993, see column 34, lines 32-48.	1-16
Y	Nucleic Acids Research, Volume 18, Number 4, issued 1990, McCarrey, "Molecular evolution of the human Pgk-2 retroposon", pages 949-955, see entire document.	1-16
Y	Japanese Journal of Cancer Research, Volume 80, issued March 1989, Kamiya et al., "Transformation of NIH3T3 Cells with Synthetic c-Ha-ras Genes", pages 200-203, see entire document.	1-16

Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	
"A"	document defining the general state of the art which is not considered to be of particular relevance
"E"	earlier document published on or after the international filing date
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"O"	document referring to an oral disclosure, use, exhibition or other means
"P"	document published prior to the international filing date but later than the priority date claimed
"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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"Z"	document member of the same patent family

Date of the actual completion of the international search

24 OCTOBER 1995

Date of mailing of the international search report

03 NOV 1995

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INTERNATIONAL SEARCH REPORT

In. National application No.
PCT/US95/11511

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Nucleic Acids Research, Volume 16, Number 17, issued 1988, Sharp et al., "Codon usage patterns in <i>Escherichia coli</i> , <i>Bacillus subtilis</i> , <i>Saccharomyces cerevisiae</i> , <i>Schizosaccharomyces pombe</i> , <i>Drosophila melanogaster</i> and <i>Homo sapiens</i> ; a review of the considerable within-species diversity", pages 8207-8211, see entire document.	1-16
Y	Proceedings of the National Academy of Sciences USA, Volume 83, issued November 1986, Newgard et al., "Sequence analysis of the cDNA encoding human liver glycogen phosphorylase reveals tissue-specific codon usage", pages 8132-8136, see entire document.	1-16
Y	Gene, Volume 46, issued 1986, Coulombe et al., "Expression of a synthetic human interferon- α , gene with modified nucleotide sequence in mammalian cells", pages 89-95, see entire document.	1-16

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/11511

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

C12N 15/09, 15/12, 15/33, 15/64

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

536/23.5, 23.72; 435/172.3

B. FIELDS SEARCHED

Minimum documentation searched

Classification System: U.S.

536/23.5, 23.72; 435/172.3

B. FIELDS SEARCHED

Documentation other than minimum documentation that are included in the fields searched:

NONE

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS. MEDLINE EXPRESS

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